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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:19:55 ; Search time 24 Seconds

(without alignments)  
560.261 Million cell updates/sec

Title: US-09-775-964-5

Perfect score: 2398  
Sequence: 1 PTDLFTNIGPDTRVWAP.....LVTLPHPNLHGPEILDVPST 457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

otal number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2398	100.0	457	4	US-09-366-009-5
2	2257	94.1	432	1	US-07-959-369-8
3	2257	94.1	432	2	US-08-836-854-20
4	2257	94.1	432	1	US-09-366-009-4
5	2254	94.0	432	1	US-07-959-369-9
6	1536.5	64.1	574	2	US-08-836-854-21
7	1536.5	64.1	574	4	US-09-463-296-1
8	1537	63.7	489	4	US-09-366-009-24
9	1499	62.5	2231	1	US-08-153-799-16
10	1485.5	61.9	302	2	US-08-836-854-5
11	1485.5	61.9	302	4	US-09-366-009-29
12	1485.5	61.9	302	1	US-08-283-857-1
13	1474	61.5	2324	4	PCT-US95-09819-1
14	1474	61.5	2324	6	5455158-1
15	1474	61.5	2386	2	US-09-016-366A-12
16	1474	61.5	2446	2	US-08-551-356-2
17	1474	61.5	2446	5	PCT-US93-12687-2
18	1463.5	61.0	472	4	US-09-366-009-21
19	1463.5	61.0	549	4	US-08-836-854-11
20	1463.5	61.0	549	4	US-09-366-009-12
21	1463.5	61.0	549	4	US-08-836-854-13
22	1455	60.7	422	2	US-09-366-009-14
23	1454	60.6	826	4	US-09-366-009-14
24	1453	60.6	446	2	US-08-836-854-15
25	1450	60.4	332	2	US-08-836-854-13
26	1448.5	60.4	464	2	US-08-836-854-19
27	1448.5	60.4	464	4	US-09-366-009-7

28	1447.5	60.4	474	2	US-08-836-854-9	Sequence 9, Appl
29	1447	60.3	368	2	US-08-836-854-17	Sequence 17, Appl
30	1442	60.1	341	2	US-08-836-854-14	Sequence 14, Appl
31	1442	60.1	367	2	US-08-836-854-18	Sequence 18, Appl
32	1442	60.1	457	2	US-08-836-854-16	Sequence 16, Appl
33	1442	60.1	457	4	US-09-366-009-22	Sequence 22, Appl
34	1437	59.9	277	1	US-07-959-369-3	Sequence 3, Appl
35	1437	59.9	279	1	US-07-959-369-11	Sequence 11, Appl
36	1437	59.9	279	2	US-08-836-854-8	Sequence 8, Appl
37	1437	59.9	281	1	US-07-959-369-4	Sequence 4, Appl
38	1437	59.9	283	1	US-07-959-369-13	Sequence 13, Appl
39	1437	59.9	283	2	US-08-836-854-7	Sequence 7, Appl
40	1437	59.9	383	1	US-07-959-369-5	Sequence 5, Appl
41	1437	59.9	385	1	US-07-959-369-14	Sequence 14, Appl
42	1437	59.9	385	2	US-08-836-854-10	Sequence 10, Appl
43	1437	59.9	491	1	US-07-804-224-2	Sequence 2, Appl
44	1437	59.9	491	5	PCT-US92-10511-2	Sequence 2, Appl
45	1437	59.9	1336	2	US-08-551-356-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-09-366-009-5  
; Sequence 5, Application US/09366009  
; Patent No. 6426042  
; GENERAL INFORMATION:  
; APPLICANT: Asada, Kiyozo  
; Uemori, Takashi  
; Yeno, Takashi  
; Koyama, No. 6426042uluo  
; Hashino, Kimikazu  
; Kato, Ikunoshin  
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
; CELLS WITH RETROVIRUS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/366,009  
; FILING DATE: 02-Aug-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,156  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 294382/1995  
; FILING DATE: 13-NOV-1995  
; APPLICATION NUMBER: JP 051847/1996  
; FILING DATE: 08-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 977,6507P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-09-366-009-5

Query Match 100.0%; Score 2398; DB 4; Length 457;  
Best Local Similarity 100.0%; Pred. No. 8.8e-172;  
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTDLRFNIGPDMRVWAPPPSIDLTNPLVRSYVKNEDVAELISPSDNVAVLTNLL 60  
DB 1 PTDLRFNIGPDMRVWAPPPSIDLTNPLVRSYVKNEDVAELISPSDNVAVLTNLL 60  
QY 61 PGTREYVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDTTANSFTVHWIAPRATTIGYR 120  
DB 61 PGTREYVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDTTANSFTVHWIAPRATTIGYR 120  
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLPGTREYVSVIALNGRESPLLIGQOSTVSD 180  
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLPGTREYVSVIALNGRESPLLIGQOSTVSD 180  
QY 181 VPRDLEVVAATPSSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
DB 181 VPRDLEVVAATPSSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
QY 241 PGVDYTTVYAVNGRSDSPASSKPSISINVTETIDKPSMAGSITTLPALPEDGSGAFPP 300  
DB 241 PGVDYTTVYAVNGRSDSPASSKPSISINVTETIDKPSMAGSITTLPALPEDGSGAFPP 300  
QY 301 GHEKDPKRLCYCKNGGFRLRIHPDGRVDGVRKSDPHIKLOAERGVASIKVCANRYL 360  
DB 301 GHEKDPKRLCYCKNGGFRLRIHPDGRVDGVRKSDPHIKLOAERGVASIKVCANRYL 360  
QY 361 AMKEDGLASKKCTDCCEFEERLESNNYNTYRSKYSYVALKRTGOYKIGSKTGPQ 420  
DB 361 AMKEDGLASKKCTDCCEFEERLESNNYNTYRSKYSYVALKRTGOYKIGSKTGPQ 420  
QY 421 KATLEFPMASADELPOLVTLPHNLGPELIDVYST 457  
DB 421 KATLEFPMASADELPOLVTLPHNLGPELIDVYST 457

RESULT 2  
US-07-959-369-8  
Sequence 8, Application US/07959369  
Patent No. 5302701  
GENERAL INFORMATION:  
APPLICANT: Higetaka HASHI et al.  
TITLE OF INVENTION: No. 5302701el Functional Polypeptide  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/959,369  
FILING DATE: 19921013  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marien M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
HYPOHETICAL:  
FRAGMENT TYPE:  
ANTI-SENSE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-959-369-8  
Query Match 94.1%; Score 2257; DB 1; Length 432;  
Best Local Similarity 99.8%; Pred. No. 2.9e-161;  
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTDLRFNIGPDMRVWAPPPSIDLTNPLVRSYVKNEDVAELISPSDNVAVLTNLL 60  
DB 1 PTDLRFNIGPDMRVWAPPPSIDLTNPLVRSYVKNEDVAELISPSDNVAVLTNLL 60  
QY 61 PGTREYVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDTTANSFTVHWIAPRATTIGYR 120  
DB 61 PGTREYVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDTTANSFTVHWIAPRATTIGYR 120  
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLPGTREYVSVIALNGRESPLLIGQOSTVSD 180  
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLPGTREYVSVIALNGRESPLLIGQOSTVSD 180  
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DB 181 VPRDLEVVAATPSSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
QY 241 PGVDYTTVYAVNGRSDSPASSKPSISINVTETIDKPSMAGSITTLPALPEDGSGAFPP 300  
DB 241 PGVDYTTVYAVNGRSDSPASSKPSISINVTETIDKPSMAGSITTLPALPEDGSGAFPP 300

QY 301 GHFKDPRLCYCKNGGFFLRHPDGRVDGVREKSDPHIKILOAEERGVSIIKVCANRYL 360  
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DB 301 GHFKDPRLCYCKNGGFFLRHPDGRVDGVREKSDPHIKILOAEERGVSIIKVCANRYL 360  
QY 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420  
|  
DB 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420  
QY 421 KALFLPMSAKS 432  
|  
DB 421 KALFLPMSAKS 432

## RESULT 3

US-08-836-854-20  
; Sequence 20, Application US/08836854  
; Patent No. 5824547  
; GENERAL INFORMATION:  
; APPLICANT: HASHINO, Kimikazu  
; APPLICANT: MATSUSHITA, Hideyuki  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSECTED CELLS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,854  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/02425  
; FILING DATE: 29-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 317721/1994  
; FILING DATE: 29-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25, 618  
; REFERENCE/DOCKET NUMBER: HASHINO=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 432 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-836-854-20

Query Match 94.1%; Score 2257; DB 2; Length 432;

Best Local Similarity 99.8%; Pred. No. 2.9e-161;  
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PDLRFNTNIGPDMRYTMAPPSIDLTNPLVRSYVKNEEDVAELSTSPEDNAVLTNLL 60  
|  
DB 1 PDLRFNTNIGPDMRYTMAPPSIDLTNPLVRSYVKNEEDVAELSTSPEDNAVLTNLL 60  
QY 61 PGTEYVAVSSVVEQHESTPLRGRQKTGLDSPGIDFSIDTANSFTVHWIAPRATITGYR 120  
|  
DB 61 PGTEYVAVSSVVEQHESTPLRGRQKTGLDSPGIDFSIDTANSFTVHWIAPRATITGYR 120

QY 121 IRHHPEHSGRPREDRVPHSRNSITLTNLPGETEYVYSIYALNGREESPLLIGQOSTVSD 180  
|  
DB 121 IRHHPEHSGRPREDRVPHSRNSITLTNLPGETEYVYSIYALNGREESPLLIGQOSTVSD 180  
QY 181 VPRDLEVAATPTSLISMDPAVTVRYRITTYGETGNSPVOEFTVPGSKSTAT1SGLK 240  
|  
DB 181 VPRDLEVAATPTSLISMDPAVTVRYRITTYGETGNSPVOEFTVPGSKSTAT1SGLK 240  
QY 241 PGVDYTTTVYAVTGRGDSPPASSKPIISINRTETIDKPSMAAGSITTLPALPEDGSGAFP 300  
|  
DB 241 PGVDYTTTVYAVTGRGDSPPASSKPIISINRTETIDKPSMAAGSITTLPALPEDGSGAFP 300  
QY 301 GHFKDPRLCYCKNGGFFLRHPDGRVDGVREKSDPHIKILOAEERGVSIIKVCANRYL 360  
|  
DB 301 GHFKDPRLCYCKNGGFFLRHPDGRVDGVREKSDPHIKILOAEERGVSIIKVCANRYL 360  
QY 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420  
|  
DB 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420  
QY 421 KALFLPMSAKS 432  
|  
DB 421 KALFLPMSAKS 432

## RESULT 4

US-09-366-009-4  
; Sequence 4, Application US/09366009  
; Patent No. 6426042  
; GENERAL INFORMATION:  
; APPLICANT: Asada, Kiyozo  
; APPLICANT: Uemori, Takashi  
; APPLICANT: Ueno, Takashi  
; Koyama, No. 6426042uto  
; Hashino, Kimikazu  
; Kato, Ikunoshin  
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
; CELLS WITH RETROVIRUS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/366,009  
; FILING DATE: 02-Aug-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,156  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 294382/1995  
; FILING DATE: 13-NOV-1995  
; APPLICATION NUMBER: JP 051847/1996  
; FILING DATE: 08-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 977.6507P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 432 amino acids  
; TYPE: amino acid

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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-366-009-4

Query Match
Best Local Similarity 94.1%; Score 2257; DB 4; Length 432;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTDLRFNIGPDMRVNAPPSIDLTNFLVRSVPKNEEDVAELSPSDNAVLTNLL 60
DB 1 PTDLRFNIGPDMRVNAPPSIDLTNFLVRSVPKNEEDVAELSPSDNAVLTNLL 60
QY 61 PGTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDTANSFTVHWIAPRATTGXR 120
DB 61 PGTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDTANSFTVHWIAPRATTGXR 120
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
QY 241 PGVDYTTVYAVTGRGSPASSKPSISINYTEIDKPSMAAGSTITLPALPEDGSGAFP 300
DB 241 PGVDYTTVYAVTGRGSPASSKPSISINYTEIDKPSMAAGSTITLPALPEDGSGAFP 300
QY 301 GHFNDPKRLCYCKNGCFELRIHPDGRVGVREKSDPHIKLOAEERGVSVIKGCANRYL 360
DB 301 GHFNDPKRLCYCKNGCFELRIHPDGRVGVREKSDPHIKLOAEERGVSVIKGCANRYL 360
QY 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRGQVYKSGTGPGQ 420
DB 361 AMKEDGRLASKCVTDECFEERLESNNYNTYRSRKYTSWYVALKRGQVYKSGTGPGQ 420
QY 421 KALIFLPMASAS 432
DB 421 KALIFLPMASAS 432

RESULT 5
US-07-959-369-9
Sequence 9, Application US/07959369
Patent No. 5302701
GENERAL INFORMATION:
APPLICANT: Hidelaka Hashi et al.
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959, 369
FILING DATE: 19921013
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
MOLECULE TYPE: polypeptide
TOPOLOGY: linear
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-9

Query Match
Best Local Similarity 94.0%; Score 2254; DB 1; Length 432;
Matches 430; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTDLRFNIGPDMRVNAPPSIDLTNFLVRSVPKNEEDVAELSPSDNAVLTNLL 60
DB 1 PTDLRFNIGPDMRVNAPPSIDLTNFLVRSVPKNEEDVAELSPSDNAVLTNLL 60
QY 61 PGTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDTANSFTVHWIAPRATTGXR 120
DB 61 PGTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDTANSFTVHWIAPRATTGXR 120
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
QY 241 PGVDYTTVYAVTGRGSPASSKPSISINYTEIDKPSMAAGSTITLPALPEDGSGAFP 300
DB 241 PGVDYTTVYAVTGRGSPASSKPSISINYTEIDKPSMAAGSTITLPALPEDGSGAFP 300
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Db 241 PGVDYTIYVAVTGRGSDPASSKPIISINVRTEIDKPSMAAGSITTLPALPEDGSGAEP 300  
Qy 301 GHFDPKRLCYCKNGGFFLRHPDGRVDGVRKSDPHIKLOAEERGVASTIKGVANRYL 360  
Db 301 GHFDPKRLCYCKNGGFFLRHPDGRVDGVRKSDPHIKLOAEERGVASTIKGVANRYL 360  
Qy 361 AMKEDGRLLASCKVYDECFEERLESNNYNTYRSRKYTSWVALKRTGQYKLGSKTGFQ 420  
Db 361 AMKEDGRLLASCKVYDECFEERLESNNYNTYRSRKYTSWVALKRTGQYKLGSKTGFQ 420  
Qy 421 KAILFLPMASAS 432  
Db 421 KAILFLPMASAS 432  
RESULT 6  
US-08-836-854-21  
; Sequence 21, Application US/08836854  
; Patent No. 5824547  
GENERAL INFORMATION:  
APPLICANT: HASHINO, Kimikazu  
APPLICANT: MATSUSHITA, Hideyuki  
APPLICANT: KATO, Ikunoshin  
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836, 854  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/02425  
FILING DATE: 29-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 317721/1994  
FILING DATE: 29-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25, 618  
REFERENCE/DOCKET NUMBER: HASHINO-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 574 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-836-854-21  
Query Match 64.1%; Score 1536.5; DB 2; Length 574;  
Best Local Similarity 58.0%; Pred. No. 3.4e-107;  
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

Db 61 PCTEYVSVSSVYEOHESTPLRGOKTGLDSTGIDSDITANSFTVHWIAPRATITGVR 120  
Qy 121 IRHHEHSGRPREDRVPHSRNSITLTNLTCTEYVSVSVVAALNGEESPILLGOOSTVSD 180  
Db 121 IRHHEHSGRPREDRVPHSRNSITLTNLTCTEYVSVSVVAALNGEESPILLGOOSTVSD 180  
Qy 181 VPRDLEVAATPTSLISMDAPAVTVRRYRTYRGTTGSGNSPQOETTVPGSKSTATISGLK 240  
Db 181 VPRDLEVAATPTSLISMDAPAVTVRRYRTYRGTTGSGNSPQOETTVPGSKSTATISGLK 240  
Qy 241 PGVDYTIYVAVTGRGSDPASSKPIISINVRTEIDKPSMAAGSITTLPALPEDGSGA 297  
Db 241 PGVDYTIYVAVTGRGSDPASSKPIISINVRTEIDKPSMAAGSITTLPALPEDGSGA 297  
Qy 298 FPPGHFKDPKRLCYCKNGGFFLRHPDGRVDGVRKSDPHIKLOAEERGVASTIKGVAN 357  
Db 301 TTPN-----VOLTGRRVTP-----KEKTGPKMTINLAPDSSSVVSGLMAT 344  
Qy 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378  
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Qy 379 FFEERLESNNYNTYRS-----RKYT----- 398  
Db 402 PGVDAPVANGQTPHQRTIKPDVRSYTTGLQGTQYKIYLTLDNARSSPVVIDASTAI 461  
Qy 399 -----SWVALKRTGQY-----KLGSK-----TG- 417  
Db 462 DAPSNLRFATTPNSLIVSWOPPRARITGYIIRKPKGSPPREVVPRPRGVTEATITGL 521  
Qy 418 -PGOKAIFL-----PM--SAASDELPOLYTLPHNPHGEIILDVPT 457  
Db 522 EPGTEYTIYVALKNNQKSEPLIGRKKTDLPOLVTLPHNPHGEIILDVPT 574  
RESULT 7  
US-09-463-296-1  
; Sequence 1, Application US/09463296  
; Patent No. 6287864  
GENERAL INFORMATION:  
APPLICANT: BAGNIS, Claude  
APPLICANT: IMBERT, Anne-Marie  
APPLICANT: MANNONI, Patrice  
TITLE OF INVENTION: GENE TRANSFER METHOD WITH THE USE OF SERUM-FREE MEDIUM  
FILE REFERENCE: BAGNIS-1  
CURRENT APPLICATION NUMBER: US/09/463, 296  
CURRENT FILING DATE: 2000-01-24  
EARLIER APPLICATION NUMBER: PCT/JP98/03173  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: JP 196772/1997  
EARLIER FILING DATE: 1997-07-23  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 574  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-463-296-1  
Query Match 64.1%; Score 1536.5; DB 4; Length 574;  
Best Local Similarity 58.0%; Pred. No. 3.4e-107;  
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

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Db 121 IRHHPHFGSRPREDVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQOSTVSD 180
QY 181 VPRDLEVAATPTSLISMDAPAVTVRYRITYGETGNSPVQETVPGSKSTATISGLK 240
Db 181 VPRDLEVAATPTSLISMDAPAVTVRYRITYGETGNSPVQETVPGSKSTATISGLK 240
QY 241 PGVDYITVYAVTGRDSDPASKPISINRTETDKPSMAAGSITTL---PALPEDGSGA 297
Db 241 PGVDYITVYAVTGRDSDPASKPISINRTETDKPSMAAGSITTL---PALPEDGSGA 297
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Db 301 TPNP-----VOLTGRVAVTP-----KEKTPMKMEINLAPDSSSVVSGLMVAT 344
QY 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
Db 345 KEVSVYALAD---TLTSRAGGVVTTLENVSPRRARVTDATETTTITTSWRTKETITG 401
QY 379 FFEERLESNNYNTYRS-----RKYT----- 398
QY 402 FOYDAVPANGQPIORTIKPDVRSYITTLGLOPGTDYKIYLYTLNDNARSSPVVIDASTAI 461
Db 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
QY 418 -PGOKAILEL-----PM--SASDELPLQVTLPHPNLHGPELIDVPST 457
Db 522 EPGETEYIVIALKNKNOSEPLIGRKKTDLPOLVTLPHPNLHGPELIDVPST 574

RESULT 8
US-09-366-009-24
; Sequence 24, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; FILING DATE: 08/809,156
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 08-MAR-1996
; APPLICATION NUMBER: JP 051847/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977,6507P
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-366-009-24

Query Match
Best Local Similarity 58.0%; Pred No. 3.4e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PTDLRTNIGPPTMRVYMAPPSIDLTFNLFVRSYVKNEDVYAEUSISPSDNVYLTNLL 60
Db 1 PTDLRTNIGPPTMRVYMAPPSIDLTFNLFVRSYVKNEDVYAEUSISPSDNVYLTNLL 60
QY 61 PCTEYVSVSVYEOHESTPLRGKQKTGLDSDPTGIDFSDITANSPTVHVIARATITGYR 120
Db 61 PCTEYVSVSVYEOHESTPLRGKQKTGLDSDPTGIDFSDITANSPTVHVIARATITGYR 120
QY 121 IRHHPHFGSRPREDVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQOSTVSD 180
Db 121 IRHHPHFGSRPREDVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQOSTVSD 180
QY 181 VPRDLEVAATPTSLISMDAPAVTVRYRITYGETGNSPVQETVPGSKSTATISGLK 240
Db 181 VPRDLEVAATPTSLISMDAPAVTVRYRITYGETGNSPVQETVPGSKSTATISGLK 240
QY 241 PGVDYITVYAVTGRDSDPASKPISINRTETDKPSMAAGSITTL---PALPEDGSGA 297
Db 241 PGVDYITVYAVTGRDSDPASKPISINRTETDKPSMAAGSITTL---PALPEDGSGA 297
QY 298 FPGHFKDPKRLYCKNGGFLRIHPDGRVGVREKSDPHIKIQLQAEBCGVASIKGVAN 357
Db 301 TPNP-----VOLTGRVAVTP-----KEKTPMKMEINLAPDSSSVVSGLMVAT 344
QY 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
Db 345 KEVSVYALAD---TLTSRAGGVVTTLENVSPRRARVTDATETTTITTSWRTKETITG 401
QY 379 FFEERLESNNYNTYRS-----RKYT----- 398
Db 402 FOYDAVPANGQPIORTIKPDVRSYITTLGLOPGTDYKIYLYTLNDNARSSPVVIDASTAI 461
QY 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
Db 522 EPGETEYIVIALKNKNOSEPLIGRKKTDLPOLVTLPHPNLHGPELIDVPST 574

RESULT 9
US-09-366-009-8
; Sequence 8, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES

```

STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/366,009  
FILING DATE: 02-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,156  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 294382/1995  
FILING DATE: 13-NOV-1995  
APPLICATION NUMBER: JP 051847/1996  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 977.6507P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-366-009-8  
Query Match 63.7%; Score 1527; DB 4; Length 489;  
Best Local Similarity 65.5%; Pred. No. 1.4e-106;  
Matches 342; Conservative 7; Mismatches 75; Indels 98; Gaps 11;  
QY 1 PTDLFTNIGPDMRYMTWAPPSPIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 60  
DB 1 PTDLFTNIGPDMRYMTWAPPSPIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 60  
QY 61 PETEVYVSVSYEQHESTPLRGROKGTGDSPTGIDFSDTANSFTVMIAPRATITGYR 120  
b 61 PETEVYVSVSYEQHESTPLRGROKGTGDSPTGIDFSDTANSFTVMIAPRATITGYR 120  
QY 121 IHHHEHFGREDRVRHSRNSITTTNTPGTVEYVSVIALNGRESPLLTGQOSTVSD 180  
DB 121 IHHHEHFGREDRVRHSRNSITTTNTPGTVEYVSVIALNGRESPLLTGQOSTVSD 180  
QY 181 VRDLEVVAAATPSTLLISMDAPAVYRYRITYGETGNSPYOEFTVPKSKSTATISGLK 240  
DB 181 VRDLEVVAAATPSTLLISMDAPAVYRYRITYGETGNSPYOEFTVPKSKSTATISGLK 240  
QY 241 PGVDYITIVYAVTGRGDSPASSKPSISINRYTEIDKPSMA-AGSITTLPALPEDGGSG-- 296  
DB 241 PGVDYITIVYAVTGRGDSPASSKPSISINRYTEIDKPSMGIRGKGTGKGGEDGFGFGPG 300  
QY 297 -----AFPGHF-----KDKRLKCKNG-----GFLRLRH 321  
DB 301 DMGKIGDKGEIGPGRGEDGEPGRGGRGPGDGPGLGPGKCKLGVPGJGPGYGRGOG 360  
QY 322 PDGRVD-----GVREKSDPHIKLQLAEEGVVSIKVCANRYLAME--- 364  
DB 361 PKGSIGFPFPGANGKGRGTGPKGRPR-----GGRGPPGRKREPRGRTGTPKGRK 413  
QY 365 -----DGRLLASKCYTDECFFPERLESNNYNTYRSKRYTSWYVALKRTGYKLGSTGPG 419  
DB 414 GNSGGDGPAGPG-----ERGNPGPGP-----TG--FPGKPGPG 447

QY 420 QKALFLP-----MSASDELPOLVTLPHPLHGPETLDVPS 457  
DB 448 PPKGDLPGHPGORGASDELPOLVTLPHPLHGPETLDVPS 489  
RESULT 10  
US-08-153-799-16  
Sequence 16, Application US/08153799  
Patent No. 5766883  
GENERAL INFORMATION:  
APPLICANT: Ballance, David J  
APPLICANT: Goodey, Andrew R  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: R Hain Swope, BOC Health Care Inc  
STREET: 100 Mountain Avenue  
CITY: Murray Hill  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07974  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,799  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847975  
FILING DATE: 06-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8909916.2  
FILING DATE: 29-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB90/00650  
FILING DATE: 26-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/775952  
FILING DATE: 29-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Swope, R Hain  
REGISTRATION NUMBER: 24864  
REFERENCE/DOCKET NUMBER: 92H832  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 665 2400  
TELEFAX: (908) 771 6159  
TELEX: 219484  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2231 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..2231  
OTHER INFORMATION: /note= "Human fibronectin"  
US-08-153-799-16  
Query Match 62.5%; Score 1499; DB 1; Length 2231;  
Best Local Similarity 51.4%; Pred. No. 1.3e-103;  
Matches 346; Conservative 31; Mismatches 64; Indels 232; Gaps 17;  
QY 1 PTDLFTNIGPDMRYMTWAPPSPIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 60  
DB 1239 PTDLFTNIGPDMRYMTWAPPSPIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 1298

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Page 8

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Db	1299	PGETEYVSASSV	EQHESTPLRKROKTGDSPGIDPSDITANSFTVMHIAARATITGYR	1356
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Db	1359	IRHHPEHFSGRPREDRYPHRSNITLTNLPTGEYVSVIALNGRESPELLIGDOOSTVD	1418	
OY	181	VPRDLEVVAAPTSLISMDAPAVTVRYXITYTGTGNSPVOEFTVPBSKSTATISGLK	240	
Db	1419	VPRDLEVVAAPTSLISMDAPAVTVRYXITYTGTGNSPVOEFTVPBSKSTATISGLK	1478	
OY	241	PGVDYTTVAAVAGRGDSPASSKPISINRTETEDIKPSMA-----AGSITTLPA----	288	
Db	1479	PGVDYTTVAAVAGRGDSPASSKPISINRTETEDIKPSQOVTDVODNISIVMKLPPSSPV	1538	
OY	289	-----LPDDGSAGAPPBHFKDPK-----RYCKN-----	313	
Db	1539	TGRVTTTPTRKNG-----PGPTTKRACGPDQEMTLEGLOPVEYVSVYYAONPBSGESOP	1592	
OY	314	-----GGFFLIATHPDGKVDYGREKSDPHI	337	
Db	1593	LVCOTAVTTPAPPLDKFTFOVTPISLSAOMTPPDVOLITGRVRHTP-----KORTGPBK	1648	
OY	338	KLOAQAEERCVASIKGVCANRY---LANKEDDRLLASK-----CVT	375	
Db	1646	EINLAPDSSSVVSGLMWAKRYEVSYVALKD---TLTSRPAOGVVTTLENNSPRRARYT	1702	
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Db	1703	DATETTITISMRTKETETITGFODVADPANOGPIQTIKIPDRVXYTINTLOOPTDYKIYL	1762	
OY	399	-----SMYAALKRTOGY-----KLSK	415	
Db	1763	YTLUNDNRSSPVVIDASTAIDARNLNRLATTPNSLLVSMQPARRAITCIYIIKEYKPPSP	1822	
OY	416	-----TG--BGOKALFL-----PM--SAASELPOLVTLHP	444	
Db	1823	PREVYPPRPPOCVTEATITITGLEPETEYTIYIALKNNOKSEPLIGKKRIDELPOLVTLHP	1882	
OY	445	NLHGPEILDVPST	457	
Db	1883	NLHGPEILDVPST	1895	

RESULT 11  
 HS-08-836-854-5  
 Sequence 5, Application US/08836854  
 Patent No. 5824547  
 GENERAL INFORMATION:  
 APPLICANT: HASHINO, Kimikazu  
 APPLICANT: MATSUSHITA, Hideyuki  
 APPLICANT: KATO, Ikunoshin  
 TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Browdy, and Neimark  
 STREET: 419 Seventh Street N.W. Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release, #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/836, 854  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

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1 APPLICATION NUMBER: PCT/JP95/024252
2 FILING DATE: 29-NOV-1995
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 317721/1994
5 FILING DATE: 29-NOV-1994
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Brody, Roger L.
8 REGISTRATION NUMBER: 25,618
9 REFERENCE/DOCKET NUMBER: HASHINO=1
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (402) 628-5197
12 TELEFAX: (402) 737-3528
13 INFORMATION FOR SEQ ID NO: 5:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 302 amino acids
16 TYPE: amino acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: peptide
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Query Match	61.9%;	Score 1485.5;	DB 2;	Length 302;
Best Local Similarity	66.1%;	Pred. No. 9.6e-104;		
Matches 302;	Conservative 0;	Mismatches 0;	Indels 155;	Gaps 1;

Qy	1	PTDLEFRTNIGGDITKRWYMAWPPPS	IDLNFNFVLRSPVKNEDDVALS	ISPSDNAVVLNLL	60
Db	1	PTDLEFRTNIGGDITKRWYMAWPPPS	IDLNFNFVLRSPVKNEDDVALS	ISPSDNAVVLNLL	60
Qy	61	PGTEVVSVSSVYQOHESTPLRGROKQKGLDPSPTG	IDFSJDTANSFTVHMIAIPRATTITGYR		120
Db	61	PGTEVVSVSSVYQOHESTPLRGROKQKGLDPSPTG	IDFSJDTANSFTVHMIAIPRATTITGYR		120
Qy	121	IRHNEHESGPRREDRVPHSHNSITLNLNPGTEVYVS	SIYALNGREESPILLICOQSTVSD		180
Db	121	IRHNEHESGPRREDRVPHSHNSITLNLNPGTEVYVS	SIYALNGREESPILLICOQSTVSD		180
Qy	181	VPROLEVVAAPRTSLISMDPAATVRYRRTTYETG	SGNSPVQEFTEVPGSKSTATISGLK		240
Db	181	VPROLEVVAAPRTSLISMDPAATVRYRRTTYETG	SGNSPVQEFTEVPGSKSTATISGLK		240
Qy	241	PGVYTTIVVAVTORGSPASSKRTISINYRFEIDKP	PMAGSGITTLPALPEDGSGAFPP		300
Db	241	PGVYTTIVVAVTORGSPASSKRTISINYRFEIDKP	PMAGSGITTLPALPEDGSGAFPP		300
Qy	301	GHEKDPKRLYCKNGCFPLRIHPDRDVOYRKRSOP	PHIKLOLAEEKRGVSIKGCANRYL		360
Db	301	GHEKDPKRLYCKNGCFPLRIHPDRDVOYRKRSOP	PHIKLOLAEEKRGVSIKGCANRYL		360
Qy	361	AMKEDGILLASKCYTDECFFERLESNNNYNTYBSR	KTTSMYVALKRTGQYKLGSKTGPQ		420
Db	361	AMKEDGILLASKCYTDECFFERLESNNNYNTYBSR	KTTSMYVALKRTGQYKLGSKTGPQ		420
Qy	421	KALLFLPMNSAASDEL.POLVTL.PHPNLGPELIDV	PST 457		
Db	421	KALLFLPMNSAASDEL.POLVTL.PHPNLGPELIDV	PST 457		
Qy	477	-----SDLEPOLVTL.PHPNLGPELIDV	PST 302		
Db	477	-----SDLEPOLVTL.PHPNLGPELIDV	PST 302		

RESULT 12 US-09-366-009-29  
US-09-366-009-29  
Sequence 29, Application US/09366009  
Patent No 6426042  
GENERAL INFORMATION:  
APPLICANT: Asada, Kiyozo  
Uemori, Takashi  
Ueno, Takashi  
Koyama, No. 6426042nto  
Hashino, Kimikazu  
Kato, Ikunoshin  
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
CELLS WITH RETROVIRUS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:



ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/366,009  
FILING DATE: 02-Aug-1999  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,156  
FILING DATE: <unknown>  
APPLICATION NUMBER: JP 294382/1995  
FILING DATE: 13-NOV-1995  
APPLICATION NUMBER: JP 051847/1996  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 977.6507P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 302 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-366-009-29

Query Match 61.9%; Score 1485.5; DB 4; Length 302;  
Best Local Similarity 66.1%; Pred. No. 9.6e-104;  
Matches 302; Conservative 0; Mismatches 0; Indels 155; Gaps 1;

QY 1 PTDLRTNIGPDMRTMRTAAPPSSIDLTNLTFLVRSYSPVKNEDVAELISPSDNAVYLTNLL 60  
DB 1 PTDLRTNIGPDMRTMRTAAPPSSIDLTNLTFLVRSYSPVKNEDVAELISPSDNAVYLTNLL 60  
QY 61 PGTETVVSVSVEQHESTPLRGROKTGLDPTGIDFSITANSFTVHMIARATITGYR 120  
DB 61 PGTETVVSVSVEQHESTPLRGROKTGLDPTGIDFSITANSFTVHMIARATITGYR 120  
QY 121 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTETVVSIVALNGREESPLLIGQOSTVSD 180  
DB 121 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTETVVSIVALNGREESPLLIGQOSTVSD 180  
QY 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRTYGETGNSPQOETVPESKSTATISGLK 240  
DB 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRTYGETGNSPQOETVPESKSTATISGLK 240  
QY 241 PGVDITIVYAVTGRGDSPASSKPIISINRTETDKP----- 276  
DB 241 PGVDITIVYAVTGRGDSPASSKPIISINRTETDKP----- 276  
QY 301 GHFKDPKRLKCKNGGFLRIHPDGRVNDGVRKSDPHIKLQDAERGVVSIKVCANRYL 360  
DB 277 ----- 276  
QY 361 AMKEDGRLLASKCTVDECFERLESNNYNTYRSRKYTSWYALKRTGQYKLGSKTGRCQ 420  
DB 277 ----- 276  
QY 421 KALFLPMSAASDELPLQVLTLPHPNLHGPEILDVPEST 457  
DB 277 ----- 276

DB 277 -----SDELPLQVLTLPHPNLHGPEILDVPEST 302

RESULT 13  
US-08-283-857-1  
Sequence 1, Application US/08283857  
Patent No. 5792742  
GENERAL INFORMATION:  
APPLICANT: GOLD, Leslie I.  
APPLICANT: ROSTAGNO, Agueda A.  
APPLICANT: BARON, Martin  
APPLICANT: CAMPBELL, Iain D.  
APPLICANT: WILLIAMS, Michael, J.  
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA  
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,857  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/714,134  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GOLD-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2324 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-283-857-1

Query Match 61.5%; Score 1474; DB 1; Length 2324;  
Best Local Similarity 46.8%; Pred. No. 9.9e-102;  
Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

QY 1 PTDLRTNIGPDMRTMRTAAPPSSIDLTNLTFLVRSYSPVKNEDVAELISPSDNAVYLTNLL 60  
DB 1239 PTDLRTNIGPDMRTMRTAAPPSSIDLTNLTFLVRSYSPVKNEDVAELISPSDNAVYLTNLL 1298  
QY 61 PGTETVVSVSVEQHESTPLRGROKTGLDPTGIDFSITANSFTVHMIARATITGYR 120  
DB 1299 PGTETVVSVSVEQHESTPLRGROKTGLDPTGIDFSITANSFTVHMIARATITGYR 1358  
QY 121 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTETVVSIVALNGREESPLLIGQOSTVSD 180  
DB 1359 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTETVVSIVALNGREESPLLIGQOSTVSD 1418  
QY 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRTYGETGNSPQOETVPESKSTATISGLK 240  
DB 1419 VPRDLEVAAPTSLISMDAPAVTVRYRYRTYGETGNSPQOETVPESKSTATISGLK 1478  
QY 241 PGVDITIVYAVTGRGDSPASSKPIISINRTETDKP-----M 278  
DB 241 PGVDITIVYAVTGRGDSPASSKPIISINRTETDKP-----M 278

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Db 1479 PGVDYTIIVYAVTGRGDSPPASSKPIISINRYTEIDKPSQMQVTDVODNSISVKWLPSSSPV 1538
OY 279 AAGSITTLTLP----- 287
Db 1539 TGYRVYTIIPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTAIV 1598
OY 288 -----ALPEGGSGSAPF-PGHFKDPKRL 309
Db 1599 TNDIRPKGLAFTDVVDYSIKIMESPQGVSRVRYTSSPEDGIEHLFPAPDGEPTAEL 1658
OY 310 YCKNGV-----FELRIH-----PDGVR 326
Db 1659 QGLRGSSEYTSVALHDMESQPLIGTOSTAIPAPTDLKFQVPTSLSAQMTFPNVQL 1718
OY 327 DGVR-----EKSDPHIKQLQAEERGVSIGVCANRY-----LAMKEDGRLLASK----- 372
Db 1719 TGYRVYTIIPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTAIV 1775
OY 373 -----CVTDEC-----FEERLESNNNTYRS-----R 395
Db 1776 VVTLLENVSPRRARVATDATTETITISMRKTETITIGFQVDAVPANGQTPIQRTIKPDVR 1835
OY 396 KYT-----SMYVA 403
Db 1836 STYITIGLOPGTDYKIYLYTLNDNASSPVVIDASTAIDAPSNLRLATTPNLSLVWQPP 1895
OY 404 LKRTQY-----KLGSK-----TG--PGOKAILFL-----PM- 428
Db 1896 RARITGYTIIEKPKGPMKEINLAPDSSVYVSGLMATKVEVSVALKD--TLTSRPAQG 1955
OY 429 -SAASDELPLQVTLTPHPNLHGPEILDVST 457
Db 1956 GRKKTDELPLQVTLTPHPNLHGPEILDVST 1985

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RESULT 14
PCT-US95-09819-1
Sequence 1 Application PC/TUS9509819
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09819
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,857
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD-1A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid

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STRANDEDNESS: single
POPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-09819-1
Query Match
Best Local Similarity 46.8% Score 1474; DB 5; Length 2324;
Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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OY 1 PDLRFTNIGPPTMRVYTAAPPSIDLTNLFVRYSPVKNEDVAELISPSDNAVLTNLL 60
Db 1239 PDLRFTNIGPPTMRVYTAAPPSIDLTNLFVRYSPVKNEDVAELISPSDNAVLTNLL 1298
OY 61 PGTEYVSVSVYEGHESTPLGRKGTGLDSDITANSFTVHVIAPRATITGYR 120
Db 1299 PGTEYVSVSVYEGHESTPLGRKGTGLDSDITANSFTVHVIAPRATITGYR 1358
OY 121 IHHHEHESGPREDRVPHSRNSITLTLNLTGTEYVSVIVALNGREESPLIGQOSTVSD 180
Db 1359 IHHHEHESGPREDRVPHSRNSITLTLNLTGTEYVSVIVALNGREESPLIGQOSTVSD 1418
OY 181 VPRDLEVVATPTSLISMDAPAVTVRYRITYGETGSGSPQOEFTVPSKSTATISGLK 240
Db 1419 VPRDLEVVATPTSLISMDAPAVTVRYRITYGETGSGSPQOEFTVPSKSTATISGLK 1478
OY 241 PGVDYTIIVYAVTGRGDSPPASSKPIISINRYTEIDKPSQMQVTDVODNSISVKWLPSSSPV 278
Db 1479 PGVDYTIIVYAVTGRGDSPPASSKPIISINRYTEIDKPSQMQVTDVODNSISVKWLPSSSPV 1538
OY 279 AAGSITTLTLP----- 287
Db 1539 TGYRVYTIIPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTAIV 1598
OY 288 -----ALPEGGSGSAPF-PGHFKDPKRL 309
Db 1599 TNDIRPKGLAFTDVVDYSIKIMESPQGVSRVRYTSSPEDGIEHLFPAPDGEPTAEL 1658
OY 310 YCKNGV-----FELRIH-----PDGVR 326
Db 1659 QGLRGSSEYTSVALHDMESQPLIGTOSTAIPAPTDLKFQVPTSLSAQMTFPNVQL 1718
OY 327 DGVR-----EKSDPHIKQLQAEERGVSIGVCANRY-----LAMKEDGRLLASK----- 372
Db 1719 TGYRVYTIIPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTAIV 1775
OY 373 -----CVTDEC-----FEERLESNNNTYRS-----R 395
Db 1776 VVTLLENVSPRRARVATDATTETITISMRKTETITIGFQVDAVPANGQTPIQRTIKPDVR 1835
OY 396 KYT-----SMYVA 403
Db 1836 STYITIGLOPGTDYKIYLYTLNDNASSPVVIDASTAIDAPSNLRLATTPNLSLVWQPP 1895
OY 404 LKRTQY-----KLGSK-----TG--PGOKAILFL-----PM- 428
Db 1896 RARITGYTIIEKPKGPMKEINLAPDSSVYVSGLMATKVEVSVALKD--TLTSRPAQG 1955
OY 429 -SAASDELPLQVTLTPHPNLHGPEILDVST 457
Db 1956 GRKKTDELPLQVTLTPHPNLHGPEILDVST 1985

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RESULT 15
5455158-1
Patent No. 5455158
APPLICANT: VOGEL, TIKVA, LEVANON, AVIGDOR, WERBER, MOSHE M.;
GUY, RACHEL; PANET, AMOS
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
USERS AND METHODS OF PRODUCING SAME
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993

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## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 526,397

FILING DATE: 21-MAY-1990

APPLICATION NUMBER: 345,952

FILING DATE: 28-APR-1989

APPLICATION NUMBER: 291,951

FILING DATE: 29-DEC-1988

SEQ ID NO:1

LENGTH: 2327

5455158-1

## Query Match

61.5%; Score 1474; DB 6; Length 2327;

Best Local Similarity 46.8%; Pred. No. 9,9e-102;

Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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OY 1 PTDLFTNIGPTMTVTAAPPSIDLTNLFVRSPPKNEDEVAELSPSDNAVLTNLL 60
Db 1242 PTDLFTNIGPTMTVTAAPPSIDLTNLFVRSPPKNEDEVAELSPSDNAVLTNLL 1301
OY 61 PGTENVVSVSYEQHESTPLGRORGTGDSPTGIDSDITANSFTVHWIAPRATTGYR 120
Db 1302 PGTENVVSVSYEQHESTPLGRORGTGDSPTGIDSDITANSFTVHWIAPRATTGYR 1361
OY 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTENVVSIVALNGRESPLLIGQSTVSD 180
Db 1362 IRHHEHESGRREDRVPHSRNSITLTNLTPTENVVSIVALNGRESPLLIGQSTVSD 1421
OY 181 VPROLEVAAATPTSLISDAPAVVRYRITYGETGNSPVOEFTVPGSKSTATISGLK 240
Db 1422 VPROLEVAAATPTSLISDAPAVVRYRITYGETGNSPVOEFTVPGSKSTATISGLK 1481
OY 241 PCVDYTIYVAVTGRGDSPASSKSPISINRYTEIDKPS-----M 278
Db 1482 PCVDYTIYVAVTGRGDSPASSKSPISINRYTEIDKPSQMVVDVQDINSISVKMLPSSPY 1541
OY 279 AAGSITTLT----- 287
Db 1542 TGYRVTTTPKNGPGPTKTAGPDQEMTIEGLQPTVEVVSVAQNPGESQPLVQTAV 1601
OY 288 -----ALPEDGGGCAFP-PGHFKDPKRL 309
Db 1602 TNIDRPGKLAFTDVDSIKIMESPOGVSRYRVYSSPEDGIHLPAPDGEDTAEI 1661
OY 310 YCKNGC-----FELRIH-----PDGRY 326
Db 1662 QGLRPGSEYTVVVALHDMESQPLIGTOSTAIPAPTDLKTQVPTSLSAQWTPPNVOL 1721
OY 327 DGVR-----EKSDPHIKLQLOAERGVSIRKVCANRY---LAKKEDGRLASK--- 372
Db 1722 TGYRVAVTPKEKTEGPMKEINLAPDSSSVVSGIMVATKYEVSVALKD---TLTSRPAQC 1778
OY 373 -----CVTDEC-----FFERLESNNVNTYRS-----R 395
Db 1779 VVTTLENNVSPRARAVTDATEFTTITISMRKTETITNGFOVDVAPANGQPTPIQRTIKPDVR 1838
OY 396 KYT----- 403
Db 1839 SYTTIGLOGTGDKYIYTLNLDNANSSPVYIDASTAIDAPSNIURLATTNLSLVSMOPP 1898
OY 404 LKRTGOY-----KLGR-----TG-PGOKAILFL-----PM- 428
Db 1899 RARITGYIIRKPKGSPPREVVPRPRPGVTEATITGLEGTETIYIVIALKNNQKSEPLI 1958
OY 429 -SAASDELPOLYTLRPNLHGPILLDPST 457
Db 1959 GRKKTDELPOLYTLRPNLHGPILLDPST 1988
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Job time : 33 secs

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(c) 1993 - 2003 CompuGen Ltd.

protein search, using sw model

March 13, 2003, 06:03:49 ; Search time 64 Seconds

951.493 Million cell updates/sec

US-09-775-964-5  
7398

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BLOSUM62

908470 seqs, 133250620 residues

hits satisfying chosen parameters: 908470

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length: 0
length: 200000000000
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Minimum Match	0%
Maximum Match	100%

Listing first 45 summaries

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2:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT *
3:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT *
4:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT *
5:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT *
6:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT *
7:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT *
8:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT *
9:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT *
10:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT *
11:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT *
12:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT *
13:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT *
14:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT *
15:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT *
16:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT *
17:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT *
18:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT *
19:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT *
20:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT *
21:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT *
22:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT *
23:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	% Match	length	DB	ID	Description
1	2398	100.0	457	18	AAW33340		Human fibronectin
2	2257	99.1	432	18	AAK40160		Human FN/DFG fusi
3	2257	94.1	432	18	AAW33339		Human Fibroblast g
4	2257	94.1	432	19	AAV05457		Fibronectin recept
5	2245	93.6	432	14	AAAR40162		Human FN/DFG fusi
6	1536.5	64.1	574	11	AAAR00044		Fibronectin deriv.
7	1536.5	64.1	574	11	AAAR60351		Inhibitory fibron
8	1536.5	64.1	574	18	AAW33349		Oligopeptide CH-29
9	1536.5	64.1	574	18	AAW13572		Escherichia coli F
10	1536.5	64.1	574	19	AAV05453		Fibronectin recept

11	1536.5	64.1	574	20	AAW973357	Protein sequence
12	1527	63.7	489	18	AAW333333	Protein used in de
13	1523	63.5	573	15	AAAR60350	Chimeric inhibitor
14	1501	62.6	2265	22	AAAR86847	Human polypeptide
15	1485.5	61.9	302	15	AAAR60355	Chimeric inhibitor
16	1485.5	61.9	302	17	AAAR98816	Cell adhesion subs
17	1485.5	61.9	302	18	AAW333352	Oligopeptide C277-
18	1474	61.5	2324	17	AAAR92778	Human fibronectin.
19	1474	61.5	2324	23	AAAR23651	Human protein rela
20	1474	61.5	2324	23	AAU74674	Human fibronectin
21	1474	61.5	2327	8	AAU70373	Human fibronectin
22	1474	61.5	2327	12	AAAR15468	Human fibronectin.
23	1474	61.5	2328	22	AAAG68182	Fibronectin protei
24	1474	61.5	2386	19	AAAG63171	Amino acid sequenc
25	1474	61.5	2386	23	AAAO17353	Human fibronectin.
26	1474	61.5	2446	15	AAAR60021	Fibrogen- $\alpha$ .
27	1474	61.5	2446	21	AAAR90377	Human fibronectin.
28	1474	61.5	2477	20	AAAR99595	Human fibronectin.
29	1473.5	61.4	2474	22	ABG22279	Novel human diagno
30	1473	61.4	2355	22	AAAR8649	Human polypeptide
31	1473	61.4	2386	22	AAAR8648	Human polypeptide
32	1463.5	61.0	472	18	AAW333366	Oligopeptide CHV-1
33	1463.5	61.0	549	12	AAAR11970	Fibronectin analog
34	1463.5	61.0	549	15	AAAR60349	Chimeric inhibitor
35	1463.5	61.0	549	18	AAAR60348	Oligopeptide CH-27
36	1463.5	61.0	549	18	AAAR13565	Human fibronectin
37	1463.5	61.0	549	19	AAAR33565	Human fibronectin
38	1454	60.6	826	18	AAAR33445	Fibronectin recept
39	1453	60.6	454	12	AAAR15672	CH2-826 oligopepti
40	1450.5	60.5	411	13	AAAR16715	Fibronectin-spacer
41	1450	60.5	538	12	AAAR15672	Cell adhesive and
42	1450	60.5	542	15	AAAR15672	EGF-fibronectin fu
43	1448.5	60.4	464	18	AAAR33342	Chimeric inhibitor
44	1448.5	60.4	464	19	AAAR33342	Protein used in de
45	1447	60.3	368	14	AAAR15672	Fibronectin recept
					Metastasis inhibi	

## ALIGNMENTS

RESULT 1	
AAW33340	
ID	AAW33340 standard; protein; 457 AA.
XX	
AC	AAW33340;
XX	
DT	23-FEB-1998 (first entry)
DE	Human fibronectin fragment containing CS-I binding domain
XX	
KW	CS-I binding domain; human fibronectin; target cell;
XX	transfection; retroviral vector; gene therapy; cancer;
KW	viral disease; acquired immunodeficiency syndrome; AIDS.
XX	
OS	Homo sapiens.
XX	
PN	WO9718318-A1.
XX	
PD	22-MAY-1997.
XX	
PF	07-NOV-1996; 96WO-JP03254.
XX	
PR	08-MAR-1996; 96JP-0051847.
XX	
PR	13-NOV-1995; 95JP-0294382.
XX	
PA	(TAKI ) TAKARA SHUZO CO LTD.
PI	
PI	Asada K, Hashino K, Kato I, Koyama N, Uemori T;
PI	Ueno T;
XX	
DR	WPI: 1997-289294/26.
XX	
DR	N-PSDB: AAT93970.
XX	



DT 23-FEB-1998 (first entry)  
 XX Human fibroblast growth factor oligopeptide.  
 DE  
 XX  
 KW Human; fibroblast growth factor; FGF; target cell;  
 KW transfection; retroviral vector; cancer;  
 KW viral disease; acquired immunodeficiency syndrome; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09718318-A1.  
 XX  
 XX 22-MAY-1997.  
 XX  
 XX 07-NOV-1996; 96WO-JP03254.  
 XX  
 XX 08-MAR-1996; 96JP-0051847.  
 XX 13-NOV-1995; 95JP-0294382.  
 XX  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 XX Asada K, Hashino K, Kato I, Koyama N, Uemori T;  
 XX Ueno T;  
 XX WPI: 1997-289294/26.  
 XX  
 XX Method for increasing efficacy of gene transfer to target cell using  
 XX retrovirus - by infection of the target cell in the presence of a  
 XX substance which binds to the virus and a substance which binds to  
 XX the target cell  
 XX  
 XX Claim 42; Pages 94-97; 194pp; Japanese.  
 XX  
 XX The present sequence is a human fibroblast growth factor (FGF)  
 XX oligopeptide, which was used in the development of a novel method  
 XX for increasing the efficiency of gene introduction into a target  
 XX cell using a retroviral vector. The method comprises carrying out  
 XX viral infection of the target cell in the presence of a retrovirus  
 XX and target cell binding substance or substances. The method can be  
 XX used to effectively introduce genes into target cells for the gene  
 XX therapy of cancer and viral diseases, e.g. AIDS.  
 XX  
 XX Sequence 432 AA:  
 SQ  
 Query Match 94.1%; Score 2257; DB 18; Length 432;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-161;  
 Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Y 1 PTDLRTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEEDVAELISPSDNAVLTNLL 60  
 DB 1 PTDLRTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEEDVAELISPSDNAVLTNLL 60  
 QY 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 DB 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 QY 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 DB 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 QY 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 DB 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 QY 181 VRDLEEVNATPTSLISMDAPAVTVRYRYRTYGETGNSPVOEFTVPGSKSTATISGLK 240  
 DB 181 VRDLEEVNATPTSLISMDAPAVTVRYRYRTYGETGNSPVOEFTVPGSKSTATISGLK 240  
 QY 241 PGVDYTIITYAVTGRDSDPSSKSPISINYTEIDKPSMAAGSITTLPALPEDGSGAFP 300  
 DB 241 PGVDYTIITYAVTGRDSDPSSKSPISINYTEIDKPSMAAGSITTLPALPEDGSGAFP 300  
 QY 301 GHFKDKRLCYCKNGGFFLRHPDGRVDGYREKSDPHIKILOLAEEGVVSIKVCANRYL 360  
 DB 301 GHFKDKRLCYCKNGGFFLRHPDGRVDGYREKSDPHIKILOLAEEGVVSIKVCANRYL 360  
 QY 361 AKKEDRLLASKCVTDECFPERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPQ 420

DB 361 AKKEDRLLASKCVTDECFPERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPQ 420  
 QY 421 KALFLPMSAAS 432  
 DB 421 KALFLPMSAKS 432  
 RESULT 4  
 AA05457  
 ID AAY05457 standard; protein; 432 AA.  
 XX  
 XX AAY05457;  
 XX  
 XX 07-JUL-1999 (first entry)  
 XX  
 XX Fibronectin receptor targeting HIV strain C-FGF A.  
 XX  
 XX Fibronectin receptor; HIV; infection; therapy.  
 XX  
 XX Unidentified.  
 XX  
 XX JP10029952-A.  
 XX  
 XX 03-FEB-1998.  
 XX  
 XX 16-JUL-1996; 96JP-0185893.  
 XX  
 XX 16-JUL-1996; 96JP-0185893.  
 XX  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 XX WPI: 1998-163674/15.  
 XX  
 XX Control of human immunodeficiency virus infection - using  
 XX composition comprising replication defective HIV vector  
 XX  
 XX Example 3; Page 21-22; 24pp; Japanese.  
 XX  
 XX This sequence represents a fibronectin receptor that can be used in  
 XX the method of the invention. The method is for the control of human  
 XX immunodeficiency virus (HIV) infection using a composition which  
 XX comprises a functional substance which participates in the infection of  
 XX HIV. The method is used to control HIV-infection.  
 XX  
 XX Sequence 432 AA:  
 SQ  
 Query Match 94.1%; Score 2257; DB 19; Length 432;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-161;  
 Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 PTDLRTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEEDVAELISPSDNAVLTNLL 60  
 DB 1 PTDLRTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEEDVAELISPSDNAVLTNLL 60  
 QY 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 DB 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 QY 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 DB 61 PCTEYVSVSSVYEOHESTPLRGROKTGLDPTGIDSDITANSFYHWTAPRATTGYR 120  
 QY 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 DB 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 QY 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 DB 121 IRHHPEHFGSRPREDRPHSRNSITLTNLTPTGEYVSVYALNGREESPLLIGQOSTVSD 180  
 QY 181 VRDLEEVNATPTSLISMDAPAVTVRYRYRTYGETGNSPVOEFTVPGSKSTATISGLK 240  
 DB 181 VRDLEEVNATPTSLISMDAPAVTVRYRYRTYGETGNSPVOEFTVPGSKSTATISGLK 240  
 QY 241 PGVDYTIITYAVTGRDSDPSSKSPISINYTEIDKPSMAAGSITTLPALPEDGSGAFP 300  
 DB 241 PGVDYTIITYAVTGRDSDPSSKSPISINYTEIDKPSMAAGSITTLPALPEDGSGAFP 300  
 QY 301 GHFKDKRLCYCKNGGFFLRHPDGRVDGYREKSDPHIKILOLAEEGVVSIKVCANRYL 360

Db 301 GHFKDPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKQLQAEERGVVSIKVCANRYL 360  
 Qy 361 AMKEGRLILASCKVTDECEFFERLESNNNTYRSRKYTSWYVALKRTGOYKLGSKTGPQO 420  
 Db 361 AMKEGRLILASCKVTDECEFFERLESNNNTYRSRKYTSWYVALKRTGOYKLGSKTGPQO 420  
 Qy 421 KALFLPMSAAS 432  
 Db 421 KALFLPMSAKS 432

RESULT 5  
 AAR40162  
 ID AAR40162 standard; peptide: 432 AA.

XX AAR40162;  
 AC AAR40162;  
 XX 07-FEB-1994 (first entry)  
 DT  
 XX

Human FN/DFGF fusion peptide #2.

KW Human: fibronectin; FN: fibroblast cell growth factor; FGF:  
 fusion; cell adhesion; cell growth; anti-aging; cosmetics;  
 wound healing; surgery.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..277  
 FT /note= "Human FN fragment 1239-1515"  
 FT Peptide 278..432  
 FT /note= "bFGF fragment"

PN JP05178897-A.  
 XX 20-JUL-1993.

PD 05-MAR-1992; 92JP-0083220.

XX 14-OCT-1991; 91JP-0291959.

XX (TAKI ) TAKARA SHUZO CO LTD.

XX WPI: 1993-261656/33.

XX Synthetic functional polypeptide to promote wound healing, etc.  
 PT contg. cell adhesion polypeptide from fibronectin and fibroblast  
 growth factor polypeptide, opt. linked by spacer

XX Disclosure: Page 9-10; 13pp: Japanese.

XX The sequences given in AAR40158-63 represent human fibronectin (FN)  
 CC and fibroblast cell growth factor (FGF) fragments which were used in  
 CC the production of fusion polypeptides which are able to stimulate  
 CC cell adhesion and cell growth. These fusion peptides may be used  
 CC for anti-aging cosmetics and in wound healing after surgery.

XX Sequence 432 AA:

Query Match 93.6%; Score 2245; DB 14; Length 432;  
 Best Local Similarity 99.3%; Pred. No. 1.8e-160;  
 Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PTDLRRTNIGPPTMRVTAPPSIDLTNFTLVRYSPKNEEDVAELISPSDANAVYTNL 60  
 Db 1 PTDLRRTNIGPPTMRVTAPPSIDLTNFTLVRYSPKNEEDVAELISPSDANAVYTNL 60  
 Qy 61 PCTEVVSVSSVYEQHESPLGRQKTGDSPTGIDFSITANSFTVWMIARATTGTR 120  
 Db 61 PCTEVVSVSSVYEQHESPLGRQKTGDSPTGIDFSITANSFTVWMIARATTGTR 120  
 Qy 121 IHHHPHESGRPREDRVPHSRNSITLTNTPGTGVSVIVALNGREESPLLIGQOSTVSD 180  
 Db 121 IHHHPHESGRPREDRVPHSRNSITLTNTPGTGVSVIVALNGREESPLLIGQOSTVSD 180

Db 121 IHHHPHESGRPREDRVPHSRNSITLTNTPGTGVSVIVALNGREESPLLIGQOSTVSD 180  
 Qy 181 VRDLEVAATPTSLISMDAPAVRYRYRTYGTGNSPQOETVGSKTATISGLK 240  
 Db 181 VRDLEVAATPTSLISMDAPAVRYRYRTYGTGNSPQOETVGSKTATISGLK 240  
 Qy 241 PCGVDTTIVYAVTNGDSPASSKPISTINRTFIDKPSMAAGSITLPLPDEGSGAFP 300  
 Db 241 PCGVDTTIVYAVTNGDSPASSKPISTINRTFIDKPSMAAGSITLPLPDEGSGAFP 300  
 Qy 301 GHFKDPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKQLQAEERGVVSIKVCANRYL 360  
 Db 301 GHFKDPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKQLQAEERGVVSIKVCANRYL 360  
 Qy 361 AMKEGRLILASCKVTDECEFFERLESNNNTYRSRKYTSWYVALKRTGOYKLGSKTGPQO 420  
 Db 361 AMKEGRLILASCKVTDECEFFERLESNNNTYRSRKYTSWYVALKRTGOYKLGSKTGPQO 420  
 Qy 421 KALFLPMSAAS 432  
 Db 421 KALFLPMSAKS 432

RESULT 6  
 AAR08044  
 ID AAR08044 standard; protein: 574 AA.

XX AAR08044;

DT 25-FEB-1991 (first entry)

XX Fibronectin deriv. for inhibition of angiogenesis.

XX Fibronectin; heparin; angiogenesis; metastasis; tumours; prolasias;  
 KW contraceptive; retinopathy; osteoporosis; rheumatism.

OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..277  
 FT /label= FN fragment of cell-binding domain  
 FT Peptide 279..549  
 FT /label= FN fragment of heparin-binding domain

PN EP339806-A.

XX 28-NOV-1990.

XX 23-MAY-1990; 90EP-0305619.

XX 01-DEC-1989; 89JP-0310536.

XX 26-MAY-1989; 89JP-0131453.

XX (TAKA-) TAKARA SHUZO KK.

XX Taguchi Y, Ohdate Y, Kawase Y, Goto S, Fusao K, Kato I, Saiki I;  
 PI Azuma I;

DR WPI: 1990-356419/48.

XX Fibronectin deriv. - contg. cell binding and heparin-binding domains  
 PT linked via amino acid residue or peptide, used s inhibitor of  
 PT angiogenesis

PS Claim 14; page 14; 20pp: English.

CC This functional fibronectin (FN) polypeptide has the formula:  
 CC C(277)-(Met)n-H(271)-X; where C(277)= the FN cell-binding domain  
 CC fragment [Pro(1239)-Ser(1315)], H(271)= the FN heparin-binding  
 CC domain fragment [Ala(1690)-Thr(1960)], X= peptide chain of 25  
 CC residues, and n= 0 or 1. The linker amino acid, Met, can be  
 CC deleted. It is produced by recombinant methods, in large quanti-  
 CC ties and is useful in an agent for inhibiting angiogenesis. It may



CC be useful in prevention of metastasis and tumour growth, as a con-  
 CC traceptive, for the treatment of e.g. osteoporosis, retinopathy and  
 CC rheumatism and to inhibit the spread of foci in psoriasis.

XX Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 11; Length 574;  
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;  
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PDLRFTNIGPDMRYMAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60  
 DB 1 PDLRFTNIGPDMRYMAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60  
 QY 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYVHMTAPRATTIGR 120  
 DB 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYVHMTAPRATTIGR 120  
 QY 121 IRHHEPFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGRESPLLIGQSTVSD 180  
 DB 121 IRHHEPFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGRESPLLIGQSTVSD 180  
 QY 181 VRDLEVAATPTSLISMDAPAVVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
 DB 181 VRDLEVAATPTSLISMDAPAVVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
 QY 241 PGVDYITVYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297  
 DB 241 PGVDYITVYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297  
 QY 298 FPGHFKDKRKYCKNGGFELRIHPDGRVDGVRKSDPHIKILOAEERGVSIGVCAN 357  
 DB 298 FPGHFKDKRKYCKNGGFELRIHPDGRVDGVRKSDPHIKILOAEERGVSIGVCAN 357  
 QY 301 TTPN-----VOLTGVRVATP-----KEKTPMKEINLADSSSVVSGLMVAT 344  
 DB 301 TTPN-----VOLTGVRVATP-----KEKTPMKEINLADSSSVVSGLMVAT 344  
 QY 358 RY----LAMKEDGRLLASK-----CYTDEC----- 378  
 DB 358 RY----LAMKEDGRLLASK-----CYTDEC----- 378  
 QY 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401  
 DB 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401  
 QY 379 FFERLESNNYNTYRS-----RKYT----- 398  
 DB 379 FFERLESNNYNTYRS-----RKYT----- 398  
 QY 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKITYLTNDNARSSPVVIDASTAI 461  
 DB 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKITYLTNDNARSSPVVIDASTAI 461  
 QY 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417  
 DB 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417  
 QY 462 DAPSNLRFATTPNSLSLWMPPRARITGYIITYEKRGSPPREVVRPRRGVTEATITGL 521  
 DB 462 DAPSNLRFATTPNSLSLWMPPRARITGYIITYEKRGSPPREVVRPRRGVTEATITGL 521  
 QY 418 -PGOKAILEL-----PM--SAASDELPOLVTLPHPNLHGPEILDVPST 457  
 DB 418 -PGOKAILEL-----PM--SAASDELPOLVTLPHPNLHGPEILDVPST 457  
 b 522 EPGETEYTIYVIALKNQKSEPLIGRKKTDELPOLVTLPHPNLHGPEILDVPST 574

RESULT 7

AAR60351 standard; protein; 574 AA.

XX AAR60351;

XX 01-MAR-1995 (first entry)

XX Inhibitory Fibrinectin receptor affinity protein.

XX fibronectin receptor; cell adhesion activity region; abnormal cells;

XX inhibitor; affinity; treatment; diagnostic agent; AIDS; cancer;

XX autoimmune deficiency syndrome; heparin binding.

XX Chimeric Homo sapiens.

XX Key Location/Qualifiers

XX FT 255..258

XX FT Domain /label= RGDS\_motif

XX JP06172203-A.

PD 21-JUN-1994.

XX 02-DEC-1992: 92JP-0345170.

XX 02-DEC-1992: 92JP-0345170.

XX (TAKI ) TAKARA SHUZO CO LTD.

DR WPI; 1994-238664/29.

PT Fibrinectin receptor-producing an abnormal cell inhibitor -

PS useful in treatment and diagnosis of AIDS and cancer

PS Claim 1; Page 22-23; 24pp; Japanese.

CC The inhibitory polypeptide has an affinity for the FR (and is used  
 CC to derive other chimeric polypeptides: AAR60348-54), and is based on  
 CC the cell adhesion activity region of human fibrinectin. All the  
 CC peptides of the invention contain an RGDS motif. The inhibitor  
 CC can be used as a therapeutic and diagnostic agent for AIDS and  
 CC cancers. (See also AAR60343-47).

XX Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 15; Length 574;  
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;  
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PDLRFTNIGPDMRYMAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60  
 DB 1 PDLRFTNIGPDMRYMAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60  
 QY 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYVHMTAPRATTIGR 120  
 DB 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYVHMTAPRATTIGR 120  
 QY 121 IRHHEPFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGRESPLLIGQSTVSD 180  
 DB 121 IRHHEPFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGRESPLLIGQSTVSD 180  
 QY 181 VRDLEVAATPTSLISMDAPAVVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
 DB 181 VRDLEVAATPTSLISMDAPAVVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240  
 QY 241 PGVDYITVYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297  
 DB 241 PGVDYITVYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297  
 QY 298 FPGHFKDKRKYCKNGGFELRIHPDGRVDGVRKSDPHIKILOAEERGVSIGVCAN 357  
 DB 298 FPGHFKDKRKYCKNGGFELRIHPDGRVDGVRKSDPHIKILOAEERGVSIGVCAN 357  
 QY 301 TTPN-----VOLTGVRVATP-----KEKTPMKEINLADSSSVVSGLMVAT 344  
 DB 301 TTPN-----VOLTGVRVATP-----KEKTPMKEINLADSSSVVSGLMVAT 344  
 QY 358 RY----LAMKEDGRLLASK-----CYTDEC----- 378  
 DB 358 RY----LAMKEDGRLLASK-----CYTDEC----- 378  
 QY 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401  
 DB 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401  
 QY 379 FFERLESNNYNTYRS-----RKYT----- 398  
 DB 379 FFERLESNNYNTYRS-----RKYT----- 398  
 QY 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKITYLTNDNARSSPVVIDASTAI 461  
 DB 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKITYLTNDNARSSPVVIDASTAI 461  
 QY 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417  
 DB 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417  
 QY 462 DAPSNLRFATTPNSLSLWMPPRARITGYIITYEKRGSPPREVVRPRRGVTEATITGL 521  
 DB 462 DAPSNLRFATTPNSLSLWMPPRARITGYIITYEKRGSPPREVVRPRRGVTEATITGL 521  
 QY 418 -PGOKAILEL-----PM--SAASDELPOLVTLPHPNLHGPEILDVPST 457  
 DB 418 -PGOKAILEL-----PM--SAASDELPOLVTLPHPNLHGPEILDVPST 457  
 b 522 EPGETEYTIYVIALKNQKSEPLIGRKKTDELPOLVTLPHPNLHGPEILDVPST 574

RESULT 8

AAW33349 standard; protein; 574 AA.

XX AAW33349

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AC AAW33349;
XX
XX 23-FEB-1998 (first entry)
XX
XX Oligopeptide CH-296.
DE
XX Oligopeptide CH-296: target cell: transfection; retroviral vector;
KW gene therapy: cancer; viral disease;
KW acquired immunodeficiency syndrome; AIDS.
XX
XX Synthetic.
XX
XX WO9718318-A1.
XX
XX 22-MAY-1997.
XX
XX 07-NOV-1996; 96WO-JP03254.
XX
XX 08-MAR-1996; 96JP-0051847.
XX 13-NOV-1995; 95JP-0294382.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX Asada K, Hashino K, Kato I, Koyama N, Uemori T;
XX Ueno T;
XX
XX WPI; 1997-289294/26.
XX
XX Method for increasing efficacy of gene transfer to target cell using
XX retrovirus - by infection of the target cell in the presence of a
XX substance which binds to the virus and a substance which binds to
XX the target cell
XX
XX
XX Disclosure: Pages 130-133; 194pp; Japanese.
XX
XX The present sequence is the oligopeptide CH-296, which was used in
XX the development of a novel method for increasing the efficiency of
XX gene introduction into a target cell using a retroviral vector. The
XX method comprises carrying out viral infection of the target cell in
XX the presence of a retrovirus and target cell binding substance or
XX substances. The method can be used to effectively introduce genes
XX into target cells for the gene therapy of cancer and viral
XX diseases, e.g. AIDS.
XX
XX
XX Sequence 574 AA:
SQ
Query Match 64.1%; Score 1536.5; DB 18; Length 574;
Best Local Similarity 58.0%; Pred. No. 4.3e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;
QY 1 PTDLFTNIGPTMRTWAPPSIDLTNPLVRYSPYKNEEDVAELISPSDNAVYLTNLL 60
DB 1 PTDLFTNIGPTMRTWAPPSIDLTNPLVRYSPYKNEEDVAELISPSDNAVYLTNLL 60
QY 61 PGTETVVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDITANSFTVHWIAPRAITTYGR 120
DB 61 PGTETVVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDITANSFTVHWIAPRAITTYGR 120
QY 121 IRHHEHESGPRREDRVPHSRNSITLNTLPCTEYVVSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHESGPRREDRVPHSRNSITLNTLPCTEYVVSIVALNGREESPLLIGQOSTVSD 180
QY 121 IRHHEHESGPRREDRVPHSRNSITLNTLPCTEYVVSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHESGPRREDRVPHSRNSITLNTLPCTEYVVSIVALNGREESPLLIGQOSTVSD 180
QY 181 VPRDEEVVAATPTSLISIDAPAVTVRYRYTYGEGNSPYOEFVTPGSKSTATISGLK 240
DB 181 VPRDEEVVAATPTSLISIDAPAVTVRYRYTYGEGNSPYOEFVTPGSKSTATISGLK 240
QY 241 PGVDVTIYVAVTGRGDSAPSKPISINRTIIDKPSMAISITTL---PALPEGGGSGA 297
DB 241 PGVDVTIYVAVTGRGDSAPSKPISINRTIIDKPSMAIPAPDLKFTQVPTSLISAGM 300
QY 298 FPPGIFKPKRLXCKNGGFLIHDPDGRVDGVRKSDPIIKIQLOAENGGVYSIKVCAN 357
DB 298 FPPGIFKPKRLXCKNGGFLIHDPDGRVDGVRKSDPIIKIQLOAENGGVYSIKVCAN 357
QY 301 TTPN-----VLTGIRAVTP-----KEXTGPKKEINLAPDSSVAVSGLMVAT 344
DB 301 TTPN-----VLTGIRAVTP-----KEXTGPKKEINLAPDSSVAVSGLMVAT 344

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QY 358 RX-----LAMKEDGRLLASK-----CVTDEC----- 378
DB 345 KYEVSIVALKD---TLTSRPAQGVTTLENVSPRRARVTDATETTTISMTKETETIG 401
QY 379 FFERLESNNTYYS-----RKYT----- 398
DB 402 FQYDAVPANGOTPIQRTIKPDYKSTHTYGLQPTDYKIITLYLNDNARSSPVYIDASTAI 461
QY 399 -----SWYVALKRTGOY-----KLSK-----TG- 417
DB 462 DAPSNLRLATTNPNSILVWOPPARITGYIIKKEKPSPREVYPRPRGVTEATITGL 521
QY 418 -PGOKATILFL-----PM--SAASDELPLVTLPHPNLHGEILDVPST 457
DB 522 EPGTEYTIYVIALYNNOKSEPLIGRKRTDELPLVTLPHPNLHGEILDVPST 574

RESULT 9
AAW13572
ID AAW13572 standard; protein; 574 AA.
XX
XX AAW13572;
XX
XX 14-NOV-1997 (first entry)
XX
XX Escherichia coli fibronectin protein.
XX
XX
XX Immunology; haematopoietic somatic cell; vertebrate; mammal; bird;
XX amphibian; fish; reptile; mouse; human; bone marrow.
XX
XX Escherichia coli.
XX
XX WO9707670-A1.
XX
XX
XX 06-MAR-1997.
XX
XX 19-AUG-1996; 96WO-JP02312.
XX
XX 30-AUG-1995; 95JP-0221583.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX Kato I, Matsushita H;
XX
XX WPI; 1997-178821/26.
XX
XX Vertebrate immunologically tolerant to foreign proteins - produced
XX by transforming haematopoietic somatic cells with a gene encoding
XX foreign protein
XX
XX Disclosure: Page 34-37; 48pp; Japanese.
XX
XX A method has been developed for producing a vertebrate immunologically
XX tolerant to foreign proteins. The method involves: (a) transforming
XX haematopoietic somatic cells of a vertebrate with a gene encoding
XX foreign proteins, (b) producing an immunodeficient vertebrate, and (c)
XX transferring the transformed cells into the immunodeficient vertebrate.
XX The present sequence represents an Escherichia coli fibronectin protein
XX which was used as an example of the above method. The vertebrate
XX may be used in the production of foreign proteins with pharmaceutical
XX applications. They may also have potential uses as models for human
XX diseases.
XX
XX
XX Sequence 574 AA:
SQ
Query Match 64.1%; Score 1536.5; DB 18; Length 574;
Best Local Similarity 58.0%; Pred. No. 4.3e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;
QY 1 PTDLFTNIGPTMRTWAPPSIDLTNPLVRYSPYKNEEDVAELISPSDNAVYLTNLL 60
DB 1 PTDLFTNIGPTMRTWAPPSIDLTNPLVRYSPYKNEEDVAELISPSDNAVYLTNLL 60

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```

QY 61 PCTEVVSVSSVYEQHESTPLRGROKGTGIDSPGTGIDFSDITANSPTVHMIARATITGYR 120
DB 61 PCTEVVSVSSVYEQHESTPLRGROKGTGIDSPGTGIDFSDITANSPTVHMIARATITGYR 120
QY 121 IRHHEHSGRRREDRVHRSNSTILTNLTPTGETVYSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHSGRRREDRVHRSNSTILTNLTPTGETVYSIVALNGREESPLLIGQOSTVSD 180
QY 181 VPRDLEVVAAATPTSLISMADAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
DB 181 VPRDLEVVAAATPTSLISMADAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
QY 241 PGVDYTIIVYAVTGRGDSPASSKPIISINRYTEIDKPSMAAGSITTL---PALPEDGSGA 297
DB 241 PGVDYTIIVYAVTGRGDSPASSKPIISINRYTEIDKPSMAIPAPDCLKFTQVPTSLAQW 300
QY 298 FPPGHFKDPKRLCYCKNGGFLLRIHPDGRVDYREKSDPHIKLOLAEEGVYSIGVCAN 357
DB 301 TTPN-----VOLTGRVAVTP-----KEKTGPMKEINLAPDSSVVSGLMAYT 344
QY 358 RY-----LAMKEDGRLASK-----CYTDEC----- 378
DB 345 KYEVSVALKD---TLTSRPAQGVVTTLENVSPRRARVTDATETTTISWRTKETITG 401
QY 379 FFEERLESNNNTYRS-----RKYT----- 398
DB 402 FOVDAPVANGOTPIQRTIKPDVRSYITIGLOPGTDYKIYLTLDNARSSPVVIDASTAI 461
QY 399 -----SWYALKRTGOY-----KLSK-----TG- 417
DB 462 DAPSNLRLATTPNSLVSWOPPRARITGYIIKYEKPGSPREVVPRPRGVTEATITGL 521
QY 418 -PGOKAILEL-----PM--SAASDELPOLYTLPHNHLGPEILDVPST 457
DB 522 EPGTEYTIIVIALKNNQKSEPLIGRKKTDLPOLVTLPHNHLGPEILDVPST 574

RESULT 10
AAV05453
ID AAV05453 standard; protein; 574 AA.
XX
AC AAV05453;
XX
DT 07-JUL-1999 (first entry)
XX
DE Fibrinectin receptor.
XX
FW Fibrinectin receptor; HIV; infection; therapy.
XX
OS Unidentified.
XX
PN JPI0029952-A.
XX
PD 03-FEB-1998.
XX
PE 16-JUL-1996; 96JP-0185893.
XX
PR 16-JUL-1996; 96JP-0185893.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1998-163674/15.
XX
PT Control of human immunodeficiency virus infection - using
PT composition comprising replication defective HIV vector
XX
XX Claim 3; Page 11-14; 24pp; Japanese.
XX
CC This sequence represents a fibrinectin receptor that can be used in
CC the method of the invention. The method is for the control of human
CC immunodeficiency virus (HIV) infection using a composition which
CC comprises a functional substance which participates in the infection of

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CC HIV. The method is used to control HIV-infection.
XX
SQ Sequence 574 AA;
Query Match 64.1%; Score 1536.5; DB 19; Length 574;
Best Local Similarity 58.0%; Pred. No. 4.3e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PTDLRFTNIGPPTMRVTAPPSIDLTNLFVYSPKKNEDVAELISPSDNAVYLTNLL 60
DB 1 PTDLRFTNIGPPTMRVTAPPSIDLTNLFVYSPKKNEDVAELISPSDNAVYLTNLL 60
QY 61 PCTEVVSVSSVYEQHESTPLRGROKGTGIDSPGTGIDFSDITANSPTVHMIARATITGYR 120
DB 61 PCTEVVSVSSVYEQHESTPLRGROKGTGIDSPGTGIDFSDITANSPTVHMIARATITGYR 120
QY 121 IRHHEHSGRRREDRVHRSNSTILTNLTPTGETVYSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHSGRRREDRVHRSNSTILTNLTPTGETVYSIVALNGREESPLLIGQOSTVSD 180
QY 181 VPRDLEVVAAATPTSLISMADAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
DB 181 VPRDLEVVAAATPTSLISMADAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
QY 241 PGVDYTIIVYAVTGRGDSPASSKPIISINRYTEIDKPSMAAGSITTL---PALPEDGSGA 297
DB 241 PGVDYTIIVYAVTGRGDSPASSKPIISINRYTEIDKPSMAIPAPDCLKFTQVPTSLAQW 300
QY 298 FPPGHFKDPKRLCYCKNGGFLLRIHPDGRVDYREKSDPHIKLOLAEEGVYSIGVCAN 357
DB 301 TTPN-----VOLTGRVAVTP-----KEKTGPMKEINLAPDSSVVSGLMAYT 344
QY 358 RY-----LAMKEDGRLASK-----CYTDEC----- 378
DB 345 KYEVSVALKD---TLTSRPAQGVVTTLENVSPRRARVTDATETTTISWRTKETITG 401
QY 379 FFEERLESNNNTYRS-----RKYT----- 398
DB 402 FOVDAPVANGOTPIQRTIKPDVRSYITIGLOPGTDYKIYLTLDNARSSPVVIDASTAI 461
QY 399 -----SWYALKRTGOY-----KLSK-----TG- 417
DB 462 DAPSNLRLATTPNSLVSWOPPRARITGYIIKYEKPGSPREVVPRPRGVTEATITGL 521
QY 418 -PGOKAILEL-----PM--SAASDELPOLYTLPHNHLGPEILDVPST 457
DB 522 EPGTEYTIIVIALKNNQKSEPLIGRKKTDLPOLVTLPHNHLGPEILDVPST 574

RESULT 11
AAW97357
ID AAW97357 standard; peptide; 574 AA.
XX
AC AAW97357;
XX
DT 12-MAY-1999 (first entry)
XX
DE Protein sequence of the specification.
XX
FW Retrovirus; gene transfer; serum-free medium; AIDS; cancer;
XX
KW leukaemia; gene therapy.
XX
OS Homo sapiens.
XX
PN WO9905301-A1.
XX
PD 04-FEB-1999.
XX
PE 15-JUL-1998; 98WO-JP03173.
XX
PR 23-JUL-1997; 97JP-0196772.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.

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XX Baguis C, Imbert A, Mannoni P;  
 XX WPI: 1999-142951/12.  
 DR Gene transfer by retrovirus in medium containing functional  
 XX substance and optionally low-density lipoprotein - useful in medical  
 PT sciences, cell and gene engineering, particularly for treating AIDS  
 PT and cancers  
 XX  
 PS Claim 5; Page 27-30; 32pp; Japanese.  
 XX  
 CC The specification describes a method for transferring a gene into  
 CC target cells by a retrovirus using a serum-free medium. The culture  
 CC medium of the target cells is serum free and contains an effective  
 CC amount of a functional substance to elevate the gene transfer efficiency  
 CC when both the retrovirus and target cells are present together. The  
 CC gene transfer method is useful in medical sciences, cell engineering  
 CC and genetic engineering, such as in the treatment of AIDS and cancers  
 e.g. leukaemia by gene therapy.

## Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 20; Length 574;  
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;  
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PTDLFTNIGPPTMRVTMAPPPSIDLTNPLVRYSPVKNEDVAELISPSDMAVYLTNLL 60  
 DB 1 PTDLFTNIGPPTMRVTMAPPPSIDLTNPLVRYSPVKNEDVAELISPSDMAVYLTNLL 60  
 QY 61 PCTEVVSVSSYEDHESTPLRGROKTGIDSPGTIDFSITANSTVMHIAARATITGR 120  
 DB 61 PCTEVVSVSSYEDHESTPLRGROKTGIDSPGTIDFSITANSTVMHIAARATITGR 120  
 QY 121 IRHHEHFSGRREDRVPHSRNSITLNLTPCTEVVSVIVALNGEESPLLIGQOSTVSD 180  
 DB 121 IRHHEHFSGRREDRVPHSRNSITLNLTPCTEVVSVIVALNGEESPLLIGQOSTVSD 180  
 QY 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240  
 DB 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240  
 QY 241 PGVDYTIIVYAVTGRGDSFASCKPISINRYEIDKPSMAAGSITL---PALPEDGSGA 297  
 DB 241 PGVDYTIIVYAVTGRGDSFASCKPISINRYEIDKPSMAIPAPTLKFTQVPTSLAQW 300  
 QY 298 FPPGHFKDPRKRLYCKNGEFFLRHDPGRVDGVRKSDPIKIQLOAEERGVSISIGVCAN 357  
 DB 301 TTPPN-----VOLTGYRVRVTP-----KEKTGPKKEINLAPDSSVVVSGIMVAT 344  
 QY 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378  
 DB 345 KYEVSVAVALKD---TLTSRPAQGVTTILENVSPPRARATVDTETITISMTKRETTIG 401  
 QY 379 FEEELLESNNNTYS-----RKYT----- 398  
 DB 402 FOYDVPANQCFPIORTIKPDKVRSITITIGLQPGTDYKIITLYLNDNANSSPVVIDASTAI 461  
 QY 399 -----SWYVALRKFGQY-----KLQSK-----TG- 417  
 DB 462 DAPSNLRELATTPNLSLLVWOPPRARITGYIIRKPKSGSPREVVPRPRPGVTEATITGL 521  
 QY 418 -FGOKAIFL-----PW-SAASDELQOLVTLPLPHNLGPEILDVPT 457  
 DB 522 EBGTEVYTIIVALKNNOKSEPLIGRKKTDELQOLVTLPLPHNLGPEILDVPT 574

RESULT 12  
 ID AAM33343  
 XX AAM33343 standard; protein; 489 AA.  
 AC AAM33343;

XX 23-FEB-1998 (first entry)  
 DT Protein used in development of gene transfer method.  
 XX  
 DE Target cell; transfection; retroviral vector; gene therapy; cancer;  
 XX viral disease; acquired immunodeficiency syndrome; AIDS.  
 KW Synthetic.  
 OS  
 XX  
 PM WO9718318-A1.  
 PD 22-MAY-1997.  
 XX  
 PF 07-NOV-1996; 96WO-JP03254.  
 XX  
 PR 08-MAR-1996; 96JP-0051847.  
 PR 13-NOV-1995; 95JP-0294382.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 PI Asada K, Hashino K, Kato I, Koyama N, Demori T;  
 PI Ueno T;  
 DR WPI: 1997-289294/26.  
 XX  
 PT Method for increasing efficacy of gene transfer to target cell using  
 PT retrovirus - by infection of the target cell in the presence of a  
 PT substance which binds to the virus and a substance which binds to  
 PT the target cell

## Claim 45; Pages 104-107; 194pp; Japanese.

CC The present sequence was used in the development of a novel method  
 CC for increasing the efficiency of gene introduction into a target  
 CC cell using a retroviral vector. The method comprises carrying out  
 CC viral infection of the target cell in the presence of a retrovirus  
 CC and target cell binding substance or substances. The method can be  
 CC used to effectively introduce genes into target cells for the gene  
 CC therapy of cancer and viral diseases, e.g. AIDS.

## Sequence 489 AA:

Query Match 63.7%; Score 1527; DB 18; Length 489;  
 Best Local Similarity 65.5%; Pred. No. 1.8e-106;  
 Matches 342; Conservative 7; Mismatches 75; Indels 98; Gaps 11;

QY 1 PTDLFTNIGPPTMRVTMAPPPSIDLTNPLVRYSPVKNEDVAELISPSDMAVYLTNLL 60  
 DB 1 PTDLFTNIGPPTMRVTMAPPPSIDLTNPLVRYSPVKNEDVAELISPSDMAVYLTNLL 60  
 QY 61 PCTEVVSVSSYEDHESTPLRGROKTGIDSPGTIDFSITANSTVMHIAARATITGR 120  
 DB 61 PCTEVVSVSSYEDHESTPLRGROKTGIDSPGTIDFSITANSTVMHIAARATITGR 120  
 QY 121 IRHHEHFSGRREDRVPHSRNSITLNLTPCTEVVSVIVALNGEESPLLIGQOSTVSD 180  
 DB 121 IRHHEHFSGRREDRVPHSRNSITLNLTPCTEVVSVIVALNGEESPLLIGQOSTVSD 180  
 QY 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240  
 DB 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240  
 QY 241 PGVDYTIIVYAVTGRGDSFASCKPISINRYEIDKPSMA-AGSITLTPALPEDGSG- 296  
 DB 241 PGVDYTIIVYAVTGRGDSFASCKPISINRYEIDKPSMGIKGTGKEKGEDGPPGKG 300  
 QY 297 -----APPGHF-----KDKPRLYCKNG-----GFFLRH 321  
 DB 301 DMGIRGDRGEIGPGRGDPGPGKGRGPGDGLGPPGPKGLGVPGLPGVPGRG 360  
 QY 322 PDGRVD-----GVREKSDPIKIQLOAEERGVSISIGVCANRYLAKKE--- 364

Db 361 PKSGIGPGPGANGKGGKGTGPKGPPR-----GGRGPTGPRGGERGPRGIGTGKPGK 413  
 QY 365 -----DGRLLASKCVTDECFEERLESNNYNTYRSKRYTSWYALKRTGQYKLGSTGPG 419  
 Db 414 GNSGDDGPPGPPG-----ERGPNGPGP-----TG--FPGKGP 447  
 QY 420 OKAILFLP-----MSASDELPLQVTLPHPLHGPPELLDVPST 457  
 Db 448 PPGKDGLPGLPGHGGASDELPLQVTLPHPLHGPPELLDVPST 489  
 RESULT 13  
 AAR60350  
 ID AAR60350 standard; protein; 573 AA.  
 XX  
 AC AAR60350;  
 XX  
 DT 01-MAR-1995 (first entry)  
 XX  
 DE Chimeric Inhibitory Fibronectin receptor affinity protein 3.  
 XX  
 KM fibronectin receptor; cell adhesion activity region; abnormal cells;  
 KW inhibitor; affinity; treatment; diagnostic agent; AIDS; cancer;  
 KM autoimmunity deficiency syndrome; heparin binding.  
 XX  
 OS Chimeric Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 255..258  
 FT /label= RGDs\_motif  
 XX  
 PN JP06172203-A.  
 XX  
 PD 21-JUN-1994.  
 XX  
 PF 02-DEC-1992; 92JP-0345170.  
 XX  
 PR 02-DEC-1992; 92JP-0345170.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 DR WPI; 1994-238664/29.  
 XX  
 PT Fibronectin receptor-producing an abnormal cell inhibitor -  
 PT useful in treatment and diagnosis of AIDS and cancer  
 XX  
 PS Claim 1; Page 15-16; 24pp; Japanese.  
 XX  
 CC AAR60348-55 are chimeric human protein inhibitors of abnormal cells  
 CC which produce fibronectin receptors (FR). These inhibitory  
 CC polypeptides have an affinity for the FRs (and are based on AAR60356),  
 CC and are based on the cell adhesion activity region of human  
 CC fibronectin. AAR60348-53 are multifunctional and can also bind heparin.  
 CC The inhibitor can be used as a therapeutic and diagnostic agent for  
 CC AIDS and cancers. (See also AAR60343-47).  
 CC  
 XX  
 SQ Sequence 573 AA:  
 Query Match 63.5%; Score 1523; DB 15; Length 573;  
 Best Local Similarity 57.6%; Pred. No. 4,5e-106;  
 Matches 341; Conservative 26; Mismatches 71; Indels 154; Gaps 14;  
 QY 1 PDDLRTNTGPDTRMTAPPPSIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 60  
 Db 1 PDDLRTNTGPDTRMTAPPPSIDLTNPLVRSYKPNEDVAELISPSDNAVLTNLL 60  
 QY 61 PGTVEVYVSVSYEHESTPLRGKQTKGLDSPTGIDFSDITANSFTVHMATPATITGYR 120  
 Db 61 PGTVEVYVSVSYEHESTPLRGKQTKGLDSPTGIDFSDITANSFTVHMATPATITGYR 120  
 QY 121 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTEVYVSVIALNGREESPLLIGQSTVSD 180  
 Db 121 IRHHPHFSGRPREDRVPHSRNSITLTNLTGTEVYVSVIALNGREESPLLIGQSTVSD 180

QY 181 VPRDLEVAATPTSLISMDAPAVTVRYRYITVGETGNSPVQEFVPGSKSTATISGLK 240  
 Db 181 VPRDLEVAATPTSLISMDAPAVTVRYRYITVGETGNSPVQEFVPGSKSTATISGLK 240  
 QY 241 PGVDYITTYAAVYAGRSDSPASSKPSISINVTEDIDKPSM--AAGSITTLPALPEDGGSGAF 298  
 Db 241 PGVDYITTYAAVYAGRSDSPASSKPSISINVTEDIDKPSM--AAGSITTLPALPEDGGSGAF 298  
 QY 299 PEGHEKDPKRLYCKNGGFEFLRIHPDGRVDGVRKSDPHIKLQLOAERGVSITKVCANR 358  
 Db 301 PPN-----VQLTGYSRVRYTP-----KEKTPMKKEINLAPDSSSVVSGLMVATK 344  
 QY 359 Y-----LAMEKDGRLASK-----CYNDEC-----F 379  
 Db 345 YEVSYYALKD---TLTSRPAQGVVTTLENVSPRRARVDATETTTISWRTETITG 401  
 QY 380 FFERLESNNYNTYRS-----RKYT-----TG-- 417  
 Db 402 QVDAVAVANQGTPTQRTIKPDVRSYTTTGLQPGTDYKIYLTLDNMRSSPVYIDASTAID 461  
 QY 399 -----SWYVALKRTGQY-----KLGSK----- 417  
 Db 462 APSNLEFLATTPTNSLIVSQPPRARITGYTIKYEKSPPREVPPRPVGTETATITGLE 521  
 QY 418 PGOKAILFLP-----PM--SAASDELPLQVTLPHPLHGPPELLDVPST 457  
 Db 522 PGTVEYTYVIALKNKNSKEPLIGRKKTDLPVTLPHPLHGPPELLDVPST 573  
 RESULT 14  
 AAM38647  
 ID AAM38647 standard; protein; 2265 AA.  
 XX  
 AC AAM38647;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 1792.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW Leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSBO INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI: 2001-442253/47.  
 DR N-PSDB: AA157803.  
 XX

Dd	1570	TGIVVTTTPKNG	-----	PGPTKTATGAPDQTEMTIEGLQPTVEVYVVSVAOMNSGESOP	16238	
Oy	314	-----	-----	GGFFLIHPDGRVDGVRKSDPHI	337	
Dd	1624	LVQATVTTIPAPDLKFTQVTPPLSLAQMTPPNVOLTGTGRVHTP	-----	-----	KEKTGPMK 16766	
Oy	338	KLOLQABEGVYSIKGYCANRY	-----	LAMKE	-----	364
Dd	1677	EINLAPSSSVVSGELMKVATKREVSVALKIDLTSTPAAQVVTLENNSPRRARVTDAT	17366	-----	-----	365
Oy	365	-----	-----	DGRLLASKCV	-----	TDECFEERL 384
Dd	1737	ETTITISMRTKETITITGEQVDAVPANGQPTDIOITIKPDVRSYITIGLOPCTDKIYLTL	17966	-----	-----	385
Oy	385	ESN	-----	NYNTRYSR	-----	395
Dd	1797	NDNARSSPVVIDASTAIDAPSNLRLATPNSLWOMPPRARITGYIIKEKPPSPRE	18566	-----	-----	396
Oy	396	-----	-----	KYTSWVVALKRTGOYKLOSKGCP	-----	GOKALFLPMAS 432
Dd	1857	VVPRPRGVTEATITPGLEPGETEYITIVIALKN	-----	NOKSEPLIGRK	-----	KT 19010
Oy	433	DELQOLVTLPHPNLHGPBEILDVST	457	-----	-----	457

QY	1	PTDLRFTNIGDYMRAVYTWAPRPSIDLTNFIYRSPVKNEEDVABLSTSPSDMAVYLTNLL	60
Db	1	PTDLRFTNIGDYMRAVYTWAPRPSIDLTNFIYRSPVKNEEDVABLSTSPSDMAVYLTNLL	60
QY	61	PGTEYVSVSSVYEDHNESTPLRGKQKGTGLDSPTGIDFSDITANSFTYHMTAPRATTITGYR	120
Db	61	PGTEYVSVSSVYEDHNESTPLRGKQKGTGLDSPTGIDFSDITANSFTYHMTAPRATTITGYR	120
QY	121	IRHHPEHSGAPREDRVRHASNSTLTNLTNLPTEYVYSVALNGREESPILLIGOOTVSD	180
Db	121	IRHHPEHSGAPREDRVRHASNSTLTNLTNLPTEYVYSVALNGREESPILLIGOOTVSD	180
QY	181	VRDLEVVAAAPRTSLTSMDDPAATVRYRYRTTYEETGCGNSPVDEFYTPGSKSTATTISGLK	240
Db	181	VRDLEVVAAAPRTSLTSMDDPAATVRYRYRTTYEETGCGNSPVDEFYTPGSKSTATTISGLK	240
QY	241	PGVDYTTIVYAVTARGDSPPASKISISINRYREIDKPSMAAGSLTTLTLPALPEDGGSGAFP	300
Db	241	PGVDYTTIVYAVTARGDSPPASKISISINRYREIDKPSMAAGSLTTLTLPALPEDGGSGAFP	300

Page 11

Fri Mar 14 08:53:32 2003

Search completed: March 13, 2003, 08:21:14  
Job time : 74 secs

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QY 278 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 337  
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Db 1 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 60  
QY 338 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 397  
|||||  
Db 61 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 120  
QY 398 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAAS 432  
|||||  
Db 121 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAKS 155

## RESULT 5

US-09-902-460-2  
; Sequence 2, Application US/09902460  
; Publication No. US20030040042A1  
; GENERAL INFORMATION:  
; APPLICANT: FIDES, J.C.

ABRAHAM, J.D.

TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
FACTOR ANALOG

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON &amp; FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/902,460

FILING DATE: 09-Jul-2001

CLASSIFICATION: &lt;unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/098,628

FILING DATE: &lt;unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 21900-20089.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 155 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-902-460-2

Query Match 34.2%; Score 820; DB 9; Length 155;  
Best Local Similarity 99.4%; Pred. No. 5,9e-55;  
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 337  
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Db 1 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 60  
QY 338 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 397  
|||||  
Db 61 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 120

QY 398 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAAS 432  
|||||  
Db 121 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAKS 155

## RESULT 6

US-09-822-485-5  
; Sequence 5, Application US/09822485  
; Patent No. US20020001825A1  
; GENERAL INFORMATION:  
; APPLICANT: Ico, No. US20020001825A1unuki

TITLE OF INVENTION: No. US20020001825A1el Fibroblast Growth Factor-Like Polypeptid

FILE REFERENCE: 08035,0001-01000

CURRENT APPLICATION NUMBER: US/09/822,485

CURRENT FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

JOURNAL: EMBO J.

VOLUME: 5

PAGES: 2523-2528

DATE: 1986

US-09-822-485-5

Query Match 34.2%; Score 820; DB 10; Length 155;  
Best Local Similarity 99.4%; Pred. No. 5,9e-55;  
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 337  
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Db 1 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 60  
QY 338 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 397  
|||||  
Db 61 KILOAEEGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNNTYRSRY 120  
QY 398 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAAS 432  
|||||  
Db 121 TSWYVALKRTGOYKLGSKTGPQKALFLPMSAKS 155

## RESULT 7

US-09-802-365-8  
; Sequence 8, Application US/09802365  
; Patent No. US20020032153A1  
; GENERAL INFORMATION:  
; APPLICANT: Whitehouse, Martha Jo

TITLE OF INVENTION: Methods and Compositions for the

TREATMENT AND PREVENTION OF ERECTILE DYSFUNCTION

FILE REFERENCE: 1671.003

CURRENT APPLICATION NUMBER: US/09/802,365

CURRENT FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/188,480

PRIOR FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 60/203,415

PRIOR FILING DATE: 2000-05-11

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-802-365-8

Query Match 34.2%; Score 820; DB 10; Length 155;  
Best Local Similarity 99.4%; Pred. No. 5,9e-55;  
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHI 337

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Db 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 120
QY 398 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 155

RESULT 8
US-09-251-263-10
; Sequence 10, Application US/09251263
; Patent No. US20020052477A1
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; FILE REFERENCE: 07265/047003
; CURRENT APPLICATION NUMBER: US/09/251,263
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 08/867,471
; EARLIER FILING DATE: 1997-06-02
; EARLIER APPLICATION NUMBER: 08/439,725
; EARLIER FILING DATE: 1995-05-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-251-263-10

Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 120
QY 398 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 155

RESULT 9
US-09-425-021-10
; Sequence 10, Application US/09425021
; Patent No. US20020076748A1
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF20301
; CURRENT APPLICATION NUMBER: US/09/425,021
; EARLIER FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 09/103,079
; EARLIER FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-425-021-10
Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 120
QY 398 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 155

RESULT 10
US-09-886-856-8
; Sequence 8, Application US/09886856
; Patent No. US20020115603A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha Jo
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Treatment of Peripheral Artery Disease
; FILE REFERENCE: PPI6090.004
; CURRENT APPLICATION NUMBER: US/09/886,856
; EARLIER FILING DATE: 2001-06-21
; EARLIER APPLICATION NUMBER: 60/213,504
; EARLIER FILING DATE: 2000-06-22
; EARLIER APPLICATION NUMBER: 60/264,572
; EARLIER FILING DATE: 2000-01-26
; EARLIER APPLICATION NUMBER: 60/276,549
; EARLIER FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-856-8

Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRY 120
QY 398 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPCKATILFLPMSAAS 155

RESULT 11
US-09-749-728B-7
; Sequence 7, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihito
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Ogawa, Keiichi
; APPLICANT: Sakurada, Kazuhito
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
```



Fri Mar 14 08:53:33 2003

us-09-775-964-5.1apb

Page 6

Best Local Similarity 98.1%; Pred. No. 2.8e-54;  
Matches 152; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 278 MAGSITTLPALPEDGSGAFPPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHI 337  
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Db 1 MAGSITTLPALPEDGSGAFPPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHI 60  
OY 338 KLOLQAEERGVSIVKGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNYNTYRSRY 397  
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Db 61 KLOLQAEERGVSIVKGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNYNTYRSRY 120  
OY 398 TSWYVALKRTGQYKLGKTPGOKALFLPMSAAS 432  
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Db 121 TSWYVALKRTGQYKLGKTPGOKALFLPMSAKS 155

RESULT 15

US-09-886-856-6  
; Sequence 6, Application US/09886856  
; Patent No. US20020115603A1

GENERAL INFORMATION:

APPLICANT: Whitehouse, Martha Jo  
; TITLE OF INVENTION: Methods and Compositions for the  
; FILE REFERENCE: Pp16090.004  
; CURRENT APPLICATION NUMBER: US/09/886,856  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/213,504  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/264,572  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/276,549  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 155  
; TYPE: prt  
; ORGANISM: Bos taurus  
US-09-886-856-6

Query Match 33.8%; Score 811; DB 10; Length 155;  
Best Local Similarity 98.1%; Pred. No. 2.8e-54;  
Matches 152; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 278 MAGSITTLPALPEDGSGAFPPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHI 337  
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Db 1 MAGSITTLPALPEDGSGAFPPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHI 60  
OY 338 KLOLQAEERGVSIVKGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNYNTYRSRY 397  
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Db 61 KLOLQAEERGVSIVKGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNYNTYRSRY 120  
OY 398 TSWYVALKRTGQYKLGKTPGOKALFLPMSAAS 432  
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Db 121 TSWYVALKRTGQYKLGKTPGOKALFLPMSAKS 155

Search completed: March 13, 2003, 11:36:40  
Job time : 27 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 07:34:37 ; Search time 39 Seconds  
(without alignments)  
1126.498 Million cell updates/sec

Title: US-09-775-964-5  
Perfect score: 2398  
Sequence: 1 PTDLRFTNIGPDTMRVTWAP.....LVTLPHPLHGPILLDVST 457

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR.73:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1474	61.5	2386	1 FNMU	fibronectin precu
2	1396	58.2	2265	1 FNBO	fibronectin - bovl
3	1345	56.1	2477	2 S14428	fibronectin precu
4	1018.5	42.5	2481	2 A43908	fibronectin - Affi
5	848	35.4	273	2 A28512	fibronectin - chic
6	824.5	34.4	210	2 A32398	basic fibroblast g
7	812	33.9	157	1 GKBOB	basic fibroblast g
8	792.5	33.0	154	2 A31674	basic fibroblast g
9	777.5	32.4	154	2 C37360	basic fibroblast g
10	768	32.0	189	2 S71465	fibronectin - chic
11	764	31.9	146	1 S00185	basic fibroblast g
12	754.5	31.5	164	2 S31622	basic fibroblast g
13	753	31.4	189	2 A48834	basic fibroblast g
14	738	30.8	137	2 I46711	fibroblast growth
15	681	28.4	155	1 A40117	basic fibroblast g
16	613.5	25.6	1020	2 A29355	fibronectin - chic
17	467	19.5	125	2 A32484	basic fibroblast g
18	425.5	17.7	155	1 A60721	acidic fibroblast
19	417.5	17.4	155	2 A60130	acidic fibroblast
20	416.5	17.4	155	1 A33665	acidic fibroblast
21	411.5	17.2	155	2 S04147	acidic fibroblast
22	411.5	17.2	155	2 D37360	acidic fibroblast
23	403.5	16.8	152	2 JH0476	acidic fibroblast
24	402.5	16.8	155	2 JH0055	acidic fibroblast
25	400.5	16.7	155	1 GKBOA	acidic fibroblast
26	378.5	15.8	1356	2 A45445	Janusin precursor,
27	358	14.9	1353	2 JH0675	restriotin precurs
28	338.5	14.1	1746	1 S19694	tenascin precursor
29	334.5	13.9	2201	2 A32160	tenascin-C - human

30	333.5	13.9	929	2 I51027	type XII collagen
31	329	13.7	1810	1 A32230	tenascin precursor
32	327	13.6	2019	1 J01322	tenascin precursor
33	309	12.9	3124	1 A40020	collagen alpha 1(X
34	302.5	12.6	4135	2 T42629	tenascin-X - bovin
35	297.5	12.4	843	2 A40970	undulin 1 - human
36	290.5	12.1	1857	2 S31212	collagen alpha 1(X
37	290.5	12.1	1888	2 S78476	collagen alpha 1(X
38	289.5	12.1	1747	1 A45974	collagen alpha 1(X
39	280.5	11.7	933	2 A31930	cytotactin - chick
40	275.5	11.5	3566	1 A40701	tenascin-X precurs
41	274	11.4	860	2 I48839	tenascin-X - mouse
42	274	11.4	4006	2 T09070	probable tenascin
43	272	11.3	2944	2 A54849	collagen alpha 1(V
44	270.5	11.3	206	1 TVDH5	fibroblast growth
45	266	11.1	194	2 T50710	fibroblast growth

## ALIGNMENTS

RESULT 1  
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fibronectin precursor [validated] - human  
N:Alternate names: fibronectin splice form ED-A  
C:Species: Homo sapiens (man)  
C:Date: 27-Nov-1985 #sequence;revision 31-Mar-1993 #text;change 08-Dec-2000  
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495;  
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987  
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.  
A:Reference number: A26460; MUID:87175578; PMID:3031656  
A:Accession: A26460  
A:Molecule type: DNA  
A:Residues: 1-49 <DEA>  
A:Cross-references: GB:M15801; NID:9182686; PIDN:AAAS376.1; PID:G553293  
R:Oldberg, A.; Ruoslahti, E.  
J. Biol. Chem. 261, 2113-2116, 1986  
A:Title: Evolution of the fibronectin gene.  
A:Reference number: A26284; MUID:86111901; PMID:3003095  
A:Accession: A26284  
A:Molecule type: DNA  
A:Residues: 1447-1540 <OLD>  
A:Cross-references: GB:M12549; NID:9182688  
A:Note: the authors translated the codon TTC for residue 1494 as Glu  
R:Paoliella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.  
Nucleic Acids Res. 16, 3545-3557, 1988  
A:Title: Sequence analysis and in vivo expression show that alternative splicing of E  
A:Reference number: S00848; MUID:88233940; PMID:3375063  
A:Accession: S03917  
A:Molecule type: DNA  
A:Residues: 1594-1767, /V/, 1769-1783 <PAO>  
A:Cross-references: EMBL:X07718; NID:931402  
A:Note: the authors translated the codon AAC for residue 1631 as Asp  
R:Viibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.  
FEBS Lett. 207, 287-291, 1986  
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin ge  
A:Reference number: A24854; MUID:87030929; PMID:3770201  
A:Accession: A24854  
A:Molecule type: DNA  
A:Residues: 1992-2147 <VIB>  
A:Cross-references: GB:X04530; NID:931436  
R:Gutman, A.; Yamada, K.M.; Kornblith, A.  
FEBS Lett. 207, 145-148, 1986  
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.  
A:Reference number: A24476; MUID:87030890; PMID:3770189  
A:Accession: A24476  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-14, /Q/, 16-38 <GUT>  
R:Kornblith, A.R.; Umezawa, K.; Viibe-Pedersen, K.; Baralle, F.E.  
EMBO J. 4, 1755-1759, 1985  
A:Title: Primary structure of human fibronectin: differential splicing may generate a

A:Reference number: A91008; MUID:85284965; PMID:2992939  
A:Accession: A91008  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 32-1344,1346-2080,2112-2386 <KOR>  
A:Cross-references: GB:X02761  
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
Nucleic Acids Res. 12, 5853-5866, 1984  
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptide  
A:Reference number: A93529; MUID:84272258; PMID:6462919  
A:Accession: A93529  
A:Molecule type: mRNA  
A:Residues: 973-2080,2112-2386 <KOR>  
A:Cross-references: GB:X00739  
R:Oldberg, A.; Linney, E.; Ruoslahti, E.  
J. Biol. Chem. 258, 10193-10196, 1983  
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell  
A:Reference number: A21011; MUID:83290929; PMID:6688418  
A:Accession: A21011  
A:Molecule type: mRNA  
A:Residues: 1454-1537 <OR2>  
A:Cross-references: GB:K00055; NID:9182680; PIDN:AAA52459.1; PID:9182683  
R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.  
Biochemistry 24, 2698-2704, 1985  
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with re  
A:Reference number: A90495; MUID:85280409; PMID:2992573  
A:Accession: A90495  
A:Molecule type: mRNA  
A:Residues: 1594-2386 <BBR>  
A:Cross-references: GB:M10905; NID:9182696; PIDN:AAA52462.1; PID:9182697  
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.  
FEBS Lett. 186, 31-34, 1985  
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.  
A:Reference number: A22245; MUID:85231203; PMID:2989004  
A:Accession: A22245  
A:Molecule type: mRNA  
A:Residues: 1948-2067 <UM2>  
A:Cross-references: GB:M27589; NID:9182705; PIDN:AAA52465.1; PID:9182706  
A:Accession: B22245  
A:Molecule type: mRNA  
A:Residues: 1975-1991,2017-2039 <UM2>  
A:Cross-references: GB:M27590  
R:Seitjunchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.  
Biochemistry 25, 4936-4941, 1986  
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes  
A:Reference number: I52394; MUID:87026578; PMID:3021206  
A:Accession: I52394  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1978-1990,2016-2018,'N',2020-2081,2113-2127 <SER>  
A:Cross-references: GB:M14060; NID:9182701; PIDN:AAA52464.1; PID:9182704  
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983  
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins  
A:Reference number: A21165; MUID:83221567; PMID:6304699  
A:Accession: A21165  
A:Molecule type: mRNA  
A:Residues: 2291-2386 <KOR>  
A:Cross-references: GB:K00799; NID:9182681; PIDN:AAA52460.1; PID:9182684  
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
J. Biol. Chem. 258, 12670-12674, 1983  
A:Title: Primary structure of human plasma fibronectin.  
A:Reference number: A52398; MUID:84032463; PMID:6630202  
A:Accession: A52398  
A:Molecule type: Protein  
A:Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>  
R:Garcia-Pardo, A.; Gold, L.I.  
Arch. Biochem. Biophys. 304, 181-188, 1993  
A:Title: Further characterization of the binding of fibronectin to gelatin reveals the F  
A:Reference number: S34791; MUID:93312001; PMID:8323285  
A:Accession: S34791  
A:Molecule type: Protein  
A:Residues: 291-300,551-560 <GAR2>

R:Griffith, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.  
Thromb. Res. 43, 469-477, 1986  
A:Title: Two plasma fibronectin fragments with different gelatin-binding properties.  
A:Reference number: A60904; MUID:87019725; PMID:3532418  
A:Accession: A60904  
A:Molecule type: Protein  
A:Residues: 293-301 <GR1>  
R:Calaycay, J.; Pardo, H.; Lee, T.; Borsl, L.; Sirl, A.; Shively, J.E.; Zardi, L.  
J. Biol. Chem. 260, 12136-12141, 1985  
A:Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human  
A:Reference number: A23901; MUID:86008277; PMID:3900070  
A:Accession: A23901  
A:Molecule type: Protein  
A:Residues: 616-677,'O',679-703,'PR' <CAL>  
R:Pierschbacher, M.D.; Ruoslahti, E.; Sundell, J.; Lind, P.; Peterson, P.A.  
J. Biol. Chem. 257, 9593-9597, 1982  
A:Title: The cell attachment domain of fibronectin. Determination of the primary stru  
A:Reference number: A52386; MUID:82265604; PMID:7050098  
A:Accession: A52386  
A:Molecule type: Protein  
A:Residues: 1441-1548 <PIE>  
A:Note: residues 1524-1527 are responsible for the cell-binding activity  
R:Garcia-Pardo, A.; Rostagno, A.; Frangione, B.  
Biochem. J. 241, 923-928, 1987  
A:Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa  
A:Reference number: A32517; MUID:87241275; PMID:3593230  
A:Accession: A32517  
A:Molecule type: Protein  
A:Residues: 1589-1630,'T',1722-2058 <GAR3>  
R:Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; P  
Biochem. J. 274, 731-738, 1991  
A:Title: Human plasma fibronectin. Demonstration of structural differences between th  
A:Reference number: S14357; MUID:91190085; PMID:2012601  
A:Accession: S14357  
A:Molecule type: Protein  
A:Residues: 1614-1630,'T',1722-2081,2113-2244 <TRE>  
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
J. Biol. Chem. 260, 10320-10325, 1985  
A:Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-  
A:Reference number: A23891; MUID:85614559; PMID:4019516  
A:Accession: A23891  
A:Molecule type: Protein  
A:Residues: 2071-2080,2112-2256 <GAR4>  
C:Comment: The extra domain and connecting strand 3 are subject to developmental and  
C:Comment: The cellular and plasma fibronectins are high molecular weight glycoprotei  
ation, and transformation.  
C:Genetics:  
A:Gene: GDB:FNI  
A:Cross-references: GDB:119135; OMIM:135600  
A:Map position: 2q34-2q34  
A:Introns: 49/3; 1266/1; 1357/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II r  
C:Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; dupl  
F:1-26/Domain: signal sequence status predicted <SIG>  
F:27-31/Domain: propeptide status predicted <PRO>  
F:32-2386/Product: fibronectin status experimental <MAT>  
F:52-272/Domain: fibrin and heparin binding <FNB>  
F:52-87/Domain: fibronectin type I repeat homology <FNB>  
F:97-135/Domain: fibronectin type I repeat homology <1F1>  
F:141-176/Domain: fibronectin type I repeat homology <1F3>  
F:186-225/Domain: fibronectin type I repeat homology <1F5>  
F:231-270/Domain: fibronectin type I repeat homology <1F5>  
F:308-608/Domain: collagen binding <CBR>  
F:308-342/Domain: fibronectin type I repeat homology <1F6>  
F:360-401/Domain: fibronectin type II repeat homology <2F1>  
F:420-461/Domain: fibronectin type II repeat homology <2F2>  
F:470-508/Domain: fibronectin type I repeat homology <1F7>  
F:518-555/Domain: fibronectin type I repeat homology <1F8>  
F:561-599/Domain: fibronectin type I repeat homology <1F9>  
F:616-692/Domain: fibronectin type III repeat homology <3FA>  
F:616-706/Domain: heparin binding <HBP>  
F:719-801/Domain: fibronectin type III repeat homology <3FB>  
F:810-891/Domain: fibronectin type III repeat homology <3FC>



F:906-988/Domain: fibronectin type III repeat homology <3FD>  
 F:996-1077/Domain: fibronectin type III repeat homology <3FE>  
 F:1086-1164/Domain: fibronectin type III repeat homology <3FE>  
 F:1173-1258/Domain: fibronectin type III repeat homology <3FG>  
 F:1266-1348/Domain: fibronectin type III repeat homology <3FH>

Query Match 61.5%; Score 1474; DB 1; Length 2386;  
 Best Local Similarity 46.8%; Pred. No. 5,6e-97;  
 Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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QY 1 PTDLFTNIGPDIMRVATWAPPSIDLNFLVRSYKKNEDVAELISDSDNAVYLTNLL 60
D 1270 PTDLFTNIGPDIMRVATWAPPSIDLNFLVRSYKKNEDVAELISDSDNAVYLTNLL 1329
QY 61 PGTEVVSVSVEQHESTPLRGROKGTLDSPGTGIDFSDITANSTVHMIAARATITGR 120
D 1330 PGTEVVSVSVEQHESTPLRGROKGTLDSPGTGIDFSDITANSTVHMIAARATITGR 1389
QY 121 IRHHEHSGRPREDRVHSHNSITLNLPGTEVVSIVALNGREESPLIGQOSTVSD 180
D 1390 IRHHEHSGRPREDRVHSHNSITLNLPGTEVVSIVALNGREESPLIGQOSTVSD 1449
QY 181 VPRDLEVAATPTSLISMDAPAVTVRYRTYGETGNSPVQEFVPGSKSTATISGLK 240
D 1450 VPRDLEVAATPTSLISMDAPAVTVRYRTYGETGNSPVQEFVPGSKSTATISGLK 1509
QY 241 PGVDYITIVAVTGRGDSPASSKPSISINVRFEIDKPS-----M 278
D 1510 PGVDYITIVAVTGRGDSPASSKPSISINVRFEIDKPSQMOVTVDNDSISVKMLDSSFPV 1569
QY 279 AAGSTITLP----- 287
D 1570 TGYRRTTPKNGPGTKTKTAGPQTEMTIEGLQPTVEVVSVAQNPSGESQPLVQTA 1629
QY 288 -----ALPEDGSGGAP-PCHEKDPKRL 309
D 1630 TNIDRPKLAFTVDVDSDIKIAMESPOGVSRVRYTSSPEDGIEHLPAPDGEEDTAL 1689
QY 310 YCKNG-----FELRIH-----PDGVR 326
D 1690 QGLRPGSEYTSVALHDMDMESQPLIGQSTAIAPPTDIKTQVPTSLSAQWTPPNVQL 1749
QY 327 DGVR-----EKSDPHIKLOAEERGVSIKVCANRY-----LAMKEDGRILASK- 372
D 1750 TGYRRTTPKNGPGTKTKTAGPQTEMTIEGLQPTVEVVSVAQNPSGESQPLVQTA 1806
QY 373 -----CYDDEC-----FFERLESNNVTYS-----R 395
D 1807 VYTLLENVSPRRARAVTATETTTITISMTKETITIGFQVDVAVPANGQTPRIQRTIKPVR 1866
QY 396 KYT-----SMVYA 403
D 1867 SYTTIGLOPGDYKIYLYTLNDNARSSPVYDASIAIDAPSNULRLATTPNLSLVWQPP 1926
QY 404 LKRTGOY-----KLGSK-----TG--PGKAILFL-----PW- 428
D 1927 RARITGIIKKKPCSSPREVVRPRPGVTEATITIGLEGTEYTIYVIALKNKNSSEPLI 1986
QY 429 -SASDELQVLTLPNHLHGPILLDVPST 457
D 1987 GRKKTDELQVLTLPNHLHGPILLDVPST 2016

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## RESULT 2

FNBO  
 fibronectin - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text\_change 20-Oct-2000  
 C:Accession: A26452; B21165; A23292  
 R:Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.  
 Eur. J. Biochem. 161, 441-453, 1986  
 A:Title: Complete primary structure of bovine plasma fibronectin.  
 A:Reference number: A26452; MUID:87054047; PMID:3780752

A:Accession: A26452  
 A:Molecule type: protein  
 A:Residues: 1-2265 <SKO>  
 R:Kornblith, A.R.; Vibe-Pedersen, K.; Balle, F.E.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983  
 A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectin  
 A:Reference number: A21165; MUID:83221567; PMID:6304699  
 A:Accession: B21165

A:Molecule type: mRNA

A:Residues: 2170-2265 <KOR>

A:Cross-references: GB:K00800; MID:9163055; PIDN:AAA0521.2; PID:95713323

R:Petersen, T.E.; Thøgersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; So  
 Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983

A:Title: Partial primary structure of bovine plasma fibronectin: three types of inter  
 A:Reference number: A23292; MUID:83117805; PMID:2218503

A:Accession: A23292

A:Molecule type: protein

A:Residues: 1-16, 'C', 18-20, 'S', 22-432, 447-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-  
 F:110-148/Domain: fibronectin type I repeat homology <1F2>  
 F:115-194/Domain: fibronectin type I repeat homology <1F3>  
 F:200-239/Domain: fibronectin type I repeat homology <1F4>  
 F:277-311/Domain: fibronectin type I repeat homology <1F5>  
 F:329-370/Domain: fibronectin type II repeat homology <2F1>  
 F:389-430/Domain: fibronectin type II repeat homology <2F2>  
 F:439-477/Domain: fibronectin type I repeat homology <1F7>  
 F:487-524/Domain: fibronectin type I repeat homology <1F8>  
 F:530-568/Domain: fibronectin type I repeat homology <1F9>  
 F:578-661/Domain: fibronectin type III repeat homology <FN3>  
 F:688-770/Domain: fibronectin type III repeat homology <FN3B>  
 F:779-860/Domain: fibronectin type III repeat homology <FN3C>  
 F:875-957/Domain: fibronectin type III repeat homology <FN3D>  
 F:965-1046/Domain: fibronectin type III repeat homology <FN3E>  
 F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>  
 F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>  
 F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>  
 F:1326-1404/Domain: fibronectin type III repeat homology <GN31>  
 F:1410-1517/Domain: cell attachment <CAD>  
 F:1493-1495/Domain: cell attachment (R-G-D) motif  
 F:1510-1592/Domain: fibronectin type III repeat homology <FN3K>  
 F:1600-1670/Domain: heparin binding <HB2>  
 F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>  
 F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>  
 F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>  
 F:1970-1972/Domain: cell attachment (R-G-D) motif  
 F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>  
 F:1985-2216/Domain: fibrin binding <FB2>  
 F:2085-2124/Domain: fibronectin type I repeat homology <1F10>  
 F:2130-2167/Domain: fibronectin type I repeat homology <1F11>  
 F:2174-2209/Domain: fibronectin type I repeat homology <1F12>  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:3/Cross-link: isopeptide (Gln) (interchain to lys N6-amino of fibrin) #status exper  
 F:21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,30  
 F:399,497,511,846,976,1213,1987/Binding site: carboxylate (Asn) (covalent) #status e  
 F:1205,1692/Binding site: carboxylate (Asn) (covalent) #status absent  
 F:1943,1944/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:2246/Disulfide bonds: interchain (to 2250) #status predicted  
 F:2250/Disulfide bonds: interchain (to 2246) #status predicted  
 F:2265/Binding site: phosphate (Ser) (covalent) #status experimental

## Query Match

58.2%; Score 1396; DB 1; Length 2265;

Best Local Similarity 48.6%; Pred. No. 2e-91;  
Matches 327; Conservative 38; Mismatches 76; Indels 232; Gaps 17;

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OY 1 PDDLRNTNIGPDMRYTAPPPSIDLTNLVRYSPVKNEDVALSTSPSDNAVLTNL 60
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OY 61 PGTVEVSVSSVEYEOHESPLRGROKTGSDPTGIDFSITTANSFTVMWIAPRATTGYR 120
OY 1299 PGTVEVSVSSVEYEOHESPLRGROKTGSDPTGIDFSITTANSFTVMWIAPRATTGYR 1358
OY 121 IRHHPHFGRRPREDVPVRSRNSITLTNLTPTGEVYVSVIALNGREESPLLIGQOSTVSD 180
OY 1359 IRHHPHFGRRPREDVPVRSRNSITLTNLTPTGEVYVSVIALNGREESPLLIGQOSTVSD 1418
OY 181 VRDLEVNATPTSLTISMDAPAVTVRYRITTYGEGTGSNPOEFTVPGSKRATISGLK 240
OY 1419 VRDLEVNATPTSLTISMDAPAVTVRYRITTYGEGTGSNPOEFTVPGSKRATISGLK 1478
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OY 1479 PGVDYITVYAVTGRDSSPSSKPSISINRTETDKPSMA-----AGSITTLPA----- 1538
OY 289 -----LPEDGSGAFPRGCHKRDK-----RLYCKN----- 313
OY 1539 TGVRYTAPKNG-----PGPSKTKVGDQDQTEMTIEGLQPTVEYVSVYAOQNGESQP 1592
OY 314 -----GGEFLRHDPGRVDGVERKSDPHI 337
OY 1593 LVQIATVTPAPTNLKTQVTPSLTAQWAPNVOLTGRRVTP-----KEKTPMK 1645
OY 338 KIQLQAEERGVSINQVCANRY-----LAKKEDGRLLASK-----CVT 375
OY 1646 EFNILAPDSSSVVSGILMAVATKVEVSYVALKD-----TLTSRPAQGVVTTLENVSPRRARYT 1702
OY 376 DEC-----FFERLESNNY-----NTRSRK 396
OY 1703 DATETTTISMTKTETITGFGVDALPANGQPTIORTIRPDVRSYTTITGLQPTGTHL 1762
OY 397 YT-----SMYVALKRTGOY-----KLGSK 415
OY 1763 YTLNDNASSPVVIDASTAIDAPSNRLATPNSLISWQPPRARITGYIIKKEPGSP 1822
OY 416 -----GCG-PGCK-----AIIFLPMSAS-----DELQVLTLPHP 444
OY 1823 PREVPRRPGVTEATITIGLEGTETTYOVALKNQKSEPLIGRKKTDLPOLVTLPH 1882
OY 445 NLHGEIILDVST 457
OY 1883 NLHGEIILDVST 1895

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## RESULT 3

SI14428 fibronectin precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Aug-1999

C:Accession: SI14428; SI12455; A22319; S46203; S00459; A27252; I59049

R:Hynes, R.O.  
submitted to the EMBL Data Library, July 1989

A:Reference number: SI14428

A:Accession: SI14428

A:Molecule type: mRNA

A:Residues: 1-2477 <HYN>

A:Cross-references: EMBL:X15906; NID:956163; PIDN:CAA34020.1; PID:956164

R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.

A:Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.

A:Reference number: SI12455; MUID:88054951; PMID:2445360

A:Accession: SI12455

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 609-1810, 'T', 1812-2283 <SCH>

A:Cross-references: EMBL:X15906  
R:Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984  
A:Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing  
A:Reference number: A22319; MUID:84298097; PMID:6089177  
A:Accession: A22319  
A:Molecule type: DNA  
A:Residues: 2052-2237 <TAM>  
R:Palckenberg, C.; Engblid, J.J.; Thøgersen, I.B.; Salvesen, G.; Akterstrom, B.  
Biochem. J. 301, 745-751, 1994  
A:Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex  
A:Reference number: S46203; MUID:94330948; PMID:7519849  
A:Accession: S46203  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1183-1192; GLN', 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'PV', 1385-1399 <PAL>  
R:Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.  
EMBO J. 6, 2565-2572, 1987  
A:Title: Organization of the fibronectin gene provides evidence for exon shuffling du  
A:Reference number: S00459; MUID:88054950; PMID:3119323  
A:Accession: S00459  
A:Molecule type: DNA  
A:Residues: 1-139; 2382-2477 <PAT>  
A:Cross-references: EMBL:X05831  
A:Note: the authors translated the codon COT for residues 51 and 94 as Ala  
R:Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.  
Cell 35, 421-431, 1983  
A:Title: Three different fibronectin mRNAs arise by alternative splicing within the c  
A:Reference number: A27252; MUID:84082067; PMID:6317187  
A:Accession: A27252  
A:Molecule type: mRNA  
A:Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>  
R:Odermatt, E.; Tamkun, J.W.; Hynes, R.O.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985  
A:Title: Repeating modular structure of the fibronectin gene: Relationship to protein  
A:Reference number: I59049; MUID:86016741; PMID:3863113  
A:Accession: I59049  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1722-1810 <RES>  
A:Cross-references: GB:M11750; NID:9204164; PIDN:AAA41170.1; PID:9554437  
A:Genetics: 51/1; 94/1; 2416/3; 2454/3  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II r  
F:1-32/Domains: alternative splicing; cell adhesion; collagen binding; disulfide bond; du  
F:33-2477/Product: fibronectin #status predicted <MAT>  
F:53-88/Domains: fibronectin type I repeat homology <LF1>  
F:98-136/Domains: fibronectin type I repeat homology <LF2>  
F:142-180/Domains: fibronectin type I repeat homology <LF3>  
F:187-226/Domains: fibronectin type I repeat homology <LF4>  
F:232-271/Domains: fibronectin type I repeat homology <LF5>  
F:308-342/Domains: fibronectin type I repeat homology <LF6>  
F:360-401/Domains: fibronectin type II repeat homology <2F1>  
F:420-461/Domains: fibronectin type II repeat homology <2F2>  
F:470-508/Domains: fibronectin type I repeat homology <LF7>  
F:518-555/Domains: fibronectin type I repeat homology <LF8>  
F:561-592/Domains: fibronectin type I repeat homology <LF9>  
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F:809-890/Domains: fibronectin type III repeat homology <FN3C>  
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F:992-1076/Domains: fibronectin type III repeat homology <FN3E>  
F:1095-1164/Domains: fibronectin type III repeat homology <FN3F>  
F:1112-1257/Domains: fibronectin type III repeat homology <FN3G>  
F:1265-1348/Domains: fibronectin type III repeat homology <FN3H>  
F:1356-1439/Domains: fibronectin type III repeat homology <FN3I>  
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F:1537-1619/Domains: fibronectin type III repeat homology <FN3K>  
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F:1631-1713/Domains: fibronectin type III repeat homology <FN3L>  
F:1721-1803/Domains: fibronectin type III repeat homology <FN3M>  
F:1811-1893/Domains: fibronectin type III repeat homology <FN3N>

F:1903-1984/Domain: fibronectin type III repeat homology <FN30>  
F:1992-2074/Domain: fibronectin type III repeat homology <FN3>  
F:2181-2183/Region: cell attachment (R-G-D) motif  
F:2193-2273/Domain: fibronectin type III repeat homology <FN30>  
F:2296-2335/Domain: fibronectin type I repeat homology <FI10>  
F:2341-2378/Domain: fibronectin type I repeat homology <FI11>  
F:2385-2420/Domain: fibronectin type I repeat homology <FI12>  
F:53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333  
368, 2366-2378, 2385-2411, 2409-2420/Disulfide bonds: #status predicted  
F:2458/Disulfide bonds: Interchain (to 2462) #status predicted  
F:2462/Disulfide bonds: Interchain (to 2458) #status predicted

Query Match 56.1%; Score 1345; DB 2; Length 2477;  
Best Local Similarity 42.4%; Pred. No. 1e-87;  
Matches 318; Conservative 49; Mismatches 87; Indels 296; Gaps 18;

Qy 1 PTDLFTNIGPDYMRVWAPPSIDLTNFLVRSPPKNEEDVAELISPSDNAVLTNLL 60  
Db 1360 PTDLFTNIGPDYMRVWAPPSIDLTNFLVRSPPKNEEDVAELISPSDNAVLTNLL 1419  
/ 61 PGTENVSSVYEQHESTPLRGROKTDGSDPTGIDFSITANSFTVHIAARATITGYR 120  
Db 1420 PGTENVSSVYEQHESTPLRGROKTDGSDPTGIDFSITANSFTVHIAARATITGYR 1479  
Qy 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTGEYVSVIALNGRESPLLIGQOSTVSD 180  
Db 1480 IRHHEHSGRPREDRVPHSRNSITLTNLTPTGEYVSVIALNGRESPLLIGQOSTVSD 1539  
Qy 181 VRDLVVAAFTPTSLISMDAPAVTVRRYRITYGTGNSPVOEFTPGSKSTATISGLK 240  
Db 1540 VRDLVVAAFTPTSLISMDAPAVTVRRYRITYGTGNSPVOEFTPGSKSTATISGLK 1599  
Qy 241 PGVDYTIIVYAVTGGDSPPASSKPSISINRTETDKP-----M 278  
Db 1600 PGVDYTIIVYAVTGGDSPPASSKPSISINRTETDKP-----M 1659  
Qy 279 AAGSTTLP----- 287  
Db 1660 TGYRTTAPKNGLGPTKSGTSPDQEMTIEGLQPTVEVSVYANRNGESQPLVQTA 1719  
Qy 288 -----ALPEDGSGAP- PGHFKDPKRL 309  
Db 1720 TNDPRKGLAFTDQVDSIKIMESPOGVSRYRVYSSPEDGIMELFPAPGDEDTABL 1779  
Qy 310 Y-----CKNGF-----FLRIH-----PDGRV 326  
Db 1780 HCLRGSEYTVSVVALLHGMESQPLIGVOSTAIPAPTNLKTQVSPFTTLTAQMTASVKL 1839  
Y 327 DQVR-----EKSDPHIKLQLOAERGVSINQVCANRY-----LAMKEDGRLASK- 372  
Db 1840 TGYRVVTPKEKTGPMKEINLSPDSITSVIVSGLMVATKYEVSVALKD---TLTSRPAG 1896  
Qy 373 -----CYTDEC-----FFERLESNNY----- 389  
Db 1897 VVTTLENNSPRRARVTAETTTITISMRTKETITIGFOVDAIPANGQTPVORTISPDVR 1956  
Qy 390 -----NTYRSKRYA-----SMVYA 403  
Db 1957 SYTTIGLOCTDYKILHLYLNDNANSSPVVDAIDAIDAPSNLRLTTTPNSILVSWQAP 2016  
Qy 404 LKRTGOY-----KLGSK-----TG--PGKAILFL-----PM- 428  
Db 2017 RARITGVIIEKPEPSPREVVRPRPGVTEATITIGLEPGTEYIVALKNNOKSEPLL 2076  
Qy 429 -SAASDELQVLTLPHPNLHGPETIDVST 457  
Db 2077 GRKKTDLPOLVTLPHPLHGPETIDVST 2106

RESULT 4  
AA3908  
Fibronectin - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 12-Feb-1999  
A:Accession: AA3908  
R:Description: D.W.: Norton, P.A.: Hynes, R.O.  
Dev. Biol. 149, 357-369, 1992  
A:Title: Identification and characterization of alternatively spliced fibronectin mRNA  
A:Reference number: AA3908; MUID:92111942; PMID:1730390  
A:Accession: AA3908  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-2481 <DES>  
A:Cross-References: GB:M77820  
A>Note: sequence extracted from NCBI backbone (NCBI:77473)  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II r  
C:Keywords: duplication; extracellular matrix; glycoprotein; heterodimer  
F:55-90/Domain: fibronectin type I repeat homology <FI1>  
F:100-138/Domain: fibronectin type I repeat homology <FI2>  
F:144-182/Domain: fibronectin type I repeat homology <FI3>  
F:189-228/Domain: fibronectin type I repeat homology <FI4>  
F:234-273/Domain: fibronectin type I repeat homology <FI5>  
F:309-343/Domain: fibronectin type I repeat homology <FI6>  
F:361-402/Domain: fibronectin type II repeat homology <FI1>  
F:421-462/Domain: fibronectin type II repeat homology <FI2>  
F:471-509/Domain: fibronectin type I repeat homology <FI7>  
F:519-556/Domain: fibronectin type I repeat homology <FI8>  
F:562-600/Domain: fibronectin type I repeat homology <FI9>  
F:610-693/Domain: fibronectin type II repeat homology <FI1>  
F:719-801/Domain: fibronectin type III repeat homology <FN3A>  
F:810-891/Domain: fibronectin type III repeat homology <FN3B>  
F:906-988/Domain: fibronectin type III repeat homology <FN3C>  
F:996-1077/Domain: fibronectin type III repeat homology <FN3D>  
F:1086-1165/Domain: fibronectin type III repeat homology <FN3E>  
F:1173-1258/Domain: fibronectin type III repeat homology <FN3F>  
F:1266-1349/Domain: fibronectin type III repeat homology <FN3G>  
F:1357-1440/Domain: fibronectin type III repeat homology <FN3I>  
F:1448-1530/Domain: fibronectin type III repeat homology <FN3J>  
F:1538-1620/Domain: fibronectin type III repeat homology <FN3K>  
F:1615-1617/Region: cell attachment (R-G-D) motif  
F:1633-1714/Domain: fibronectin type III repeat homology <FN3L>  
F:1722-1804/Domain: fibronectin type III repeat homology <FN3M>  
F:1812-1894/Domain: fibronectin type III repeat homology <FN3N>  
F:1904-1985/Domain: fibronectin type III repeat homology <FN3O>  
F:1993-2075/Domain: fibronectin type III repeat homology <FN3P>  
F:2197-2277/Domain: fibronectin type III repeat homology <FN3Q>  
F:2301-2340/Domain: fibronectin type I repeat homology <FI10>  
F:2346-2383/Domain: fibronectin type I repeat homology <FI11>  
F:2396-2425/Domain: fibronectin type I repeat homology <FI12>  
F:55-81, 79-90, 100-128, 126-138, 144-172, 170-182, 189-218, 216-228, 234-263, 261-273, 309-336  
2373, 2371-2383, 2390-2416, 2414-2425/Disulfide bonds: #status predicted  
F:2459/Disulfide bonds: Interchain (to 2463) #status predicted  
F:2463/Disulfide bonds: Interchain (to 2459) #status predicted

Query Match 42.5%; Score 1018.5; DB 2; Length 2481;  
Best Local Similarity 68.7%; Pred. No. 2.6e-64;  
Matches 195; Conservative 43; Mismatches 65; Indels 1; Gaps 1;

Qy 1 PTDLFTNIGPDYMRVWAPPSIDLTNFLVRSPPKNEEDVAELISPSDNAVLTNLL 60  
Db 1361 PTDLFTNIGPDYMRVWAPPSIDLTNFLVRSPPKNEEDVAELISPSDNAVLTNLL 1420  
Qy 61 PGTENVSSVYEQHESTPLRGROKTDGSDPTGIDFSITANSFTVHIAARATITGYR 120  
Db 1421 PGTENVSSVYEQHESTPLRGROKTDGSDPTGIDFSITANSFTVHIAARATITGYR 1480  
Qy 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTGEYVSVIALNGRESPLLIGQOSTVSD 180  
Db 1481 IRHHEHSGRPREDRVPHSRNSITLTNLTPTGEYVSVIALNGRESPLLIGQOSTVSD 1540  
Qy 181 VRDLVVAAFTPTSLISMDAPAVTVRRYRITYGTGNSPVOEFTPGSKSTATISGLK 240  
Db 1541 VRDLVVAAFTPTSLISMDAPAVTVRRYRITYGTGNSPVOEFTPGSKSTATISGLK 1600

Db 1601 PGVSITTYTAAVATGRCDSPPASSKPLTIHKTDVDDPIDNAVTDI 1644

# RESULT 5

A28512

fibronectin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 31-Dec-1988 #sequence-revision 31-Dec-1988 #text-change 20-Aug-1999

C:Accession: A28512

R:Kubomura, S.; Obata, M.; Kanasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K.

Biochem. Biophys. Acta 910, 171-181, 1987

A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin g

A:Reference number: A28512; MUID:88050950; PMID:2823899

A:Accession: A28512

A:Molecule type: DNA

A:Residues: 1-273 <KUR>

A:Cross-references: GB:J06553; NID:963393; PIDN:CAA29781.1; PID:9295716

A:Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243

C:Genetics: 90/1: 129/1: 184/1: 236/1

uperfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe

Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter

F:1-82/Domain: fibronectin type III repeat homology (fragment) <FN3I>

F:90-172/Domain: fibronectin type III repeat homology <FN3J>

F:167-169/Region: cell attachment (R-G-D) motif

F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match 35.4% Score 848; DB 2; Length 273;

Best Local Similarity 84.7% Pred. No. 1.9e-53;

Matches 160; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 89 LDPSTGIDPSDITANSTFTYVWIMAPRTTGYRIRHHPHSGSPRRDRVHNSITLTN 148

DB 1 LDPSTGIDPSDITANSTFTYVWIMAPRTTGYRIRHHPHSGSPRRDRVHNSITLTN 60

QY 149 LTFGTETVYVIVALNGRESPLILGOOSTYSDVPRDLEVAATPTSLILSMAPAVTVR 208

DB 61 LTFGTETVYVIVALNGRESPLILGOOSTYSDVPRDLEVAATPTSLILSMAPAVTVR 120

QY 209 YRTTETGNSPVOEFYVPGSKSTATISGLKPGVDYTTTVAVNTGRGSPASSKPIISN 268

DB 121 YRTTETGNSPVOEFYVPGSKSTATISGLKPGVDYTTTVAVNTGRGSPASSKPIISN 180

QY 269 YRTTETGNSPVOEFYVPGSKSTATISGLKPGVDYTTTVAVNTGRGSPASSKPIISN 277

DB 181 YRTTETGNSPVOEFYVPGSKSTATISGLKPGVDYTTTVAVNTGRGSPASSKPIISN 189

QY 398

basic fibroblast growth factor precursor, 22.5K form - human

N:Alternate names: bFGF; fibroblast growth factor 2; prostatic growth factor; prostatic

N:Contains: basic fibroblast growth factor, 18K form

C:Species: Homo sapiens (man)

C>Date: 31-Jul-1988 #sequence-revision 31-Dec-1993 #text-change 21-Jul-2000

C:Accession: A32398; A01537; A26842; B28278; S00297; A54316; B54316; A33624; A25824; B24

R:Prasas, H.; Kaghad, M.; Prasas, A.C.; Klagsbrun, M.; Lelias, J.M.; Lauzun, P.; Chalon,

Proc. Natl. Acad. Sci. U.S.A. 86, 1836-1840, 1989

A:Title: High molecular mass forms of basic fibroblast growth factor are initiated by a

A:Reference number: A32398; MUID:89184522; PMID:2538817

A:Accession: A32398

A:Molecule type: mRNA

A:Residues: 1-210 <PRA>

A:Cross-references: GB:J04513; NID:9183083; PIDN:AAA5253.1; PID:9459811

R:Shibata, F.; Balid, A.; Florkiewicz, R.Z.

Growth Factors 4, 277-287, 1991

A:Title: Functional characterization of the human basic fibroblast growth factor gene pr

A:Reference number: A61537; MUID:92110035; PMID:1764264

A:Accession: A61537

A:Molecule type: DNA

A:Residues: 1-114 <SHI>

A:Note: authors translated the codon GCA for residue 47 as Ala

R:Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.

FEBS Lett. 213, 189-194, 1987

A:Title: Cloning and expression of cDNA encoding human basic fibroblast growth factor

A:Reference number: A26642; MUID:87162468; PMID:2435575

A:Accession: A26642

A:Molecule type: mRNA

A:Residues: 56-210 <KUR>

A:Cross-references: GB:M27968; NID:9182562; PIDN:AAA52448.1; PID:9182563

R:Abraham, J.A.; Whang, J.L.; Tumolo, A.; Merz, A.; Friedmann, J.; Gospodarowicz, D.

Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986

A:Title: Human basic fibroblast growth factor: nucleotide sequence, genomic organizat

A:Reference number: A90924; MUID:87217066; PMID:3472745

A:Accession: B32878

A:Molecule type: mRNA

A:Residues: 56-210 <ABR>

A:Note: the authors translated the codon GAA for residue 108 as Gly

R:Abraham, J.A.; Whang, J.L.; Tumolo, A.; Merz, A.; Friedmann, J.; Gospodarowicz, D.

EMBO J. 5, 2523-2528, 1986

A:Title: Human basic fibroblast growth factor: nucleotide sequence and genomic organ

A:Reference number: S00297; MUID:87053817; PMID:3780670

A:Accession: S00297

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-155 <AB2>

A:Note: the authors translated the codon GAA for residue 108 as Gly

R:Shimoyama, Y.; Gotoh, M.; Ino, Y.; Sakamoto, M.; Kato, K.; Hirohashi, S.

Jpn. J. Cancer Res. 82, 1263-1270, 1991

A:Title: Characterization of high-molecular-mass forms of basic fibroblast growth fac

riogenesis.

A:Reference number: A54316; MUID:92091228; PMID:1721615

A:Accession: A54316

A:Molecule type: protein

A:Residues: 7XX, 86-88, 90-91, 93-95 <SH3>

A:Experimental source: C-121 hepatocellular carcinoma cell line

A:Note: sequence extracted from NCBI backbone (NCBI:71595)

A:Accession: B54316

A:Molecule type: protein

A:Residues: 7XX, 19, 21-29 <SH2>

A:Note: sequence extracted from NCBI backbone (NCBI:71594)

R:Feite, J.D.; Bradley, J.D.; Fryburg, K.; Faris, J.; Cousins, L.C.; Barr, P.J.; Bai

J. Cell Biol. 109, 3105-3114, 1989

A:Title: Differential effects of heparin, fibronectin, and laminin on the phosphoryla

A:Reference number: A33624; MUID:90078343; PMID:2592418

A:Accession: A33624

A>Status: preliminary

A:Molecule type: protein

A:Residues: 57-210 <PRE>

R:Story, M.T.; Esch, F.; Shimasaki, S.; Sasse, J.; Jacobs, S.C.; Lawson, R.K.

Biochem. Biophys. Res. Commun. 142, 702-709, 1987

A:Title: Amino-terminal sequence of a large form of basic fibroblast growth factor is

A:Reference number: A25824; MUID:87156686; PMID:2435284

A:Accession: A25824

A:Molecule type: protein

A:Residues: 57-77 <STO>

A:Experimental source: prostate

R:Gimenez-Gallo, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.

Biochem. Biophys. Res. Commun. 135, 541-548, 1986

A:Title: Human brain-derived acidic and basic fibroblast growth factors: amino termin

A:Reference number: A90122; MUID:86186784; PMID:3964259

A:Accession: B24243

A:Molecule type: protein

A:Residues: 65-102, 104-105 <GIM>

A:Experimental source: brain

R:Gautschi, P.; Frater-Schroder, M.; Bohlen, P.

FEBS Lett. 204, 203-207, 1986

A:Title: Partial molecular characterization of endothelial cell mitogens from human b

A:Reference number: A91364; MUID:86752560; PMID:3732516

A:Accession: B24301

A:Molecule type: protein

A:Residues: 65-88, 90-98, 100 <GUV>

R:Sommer, A.; Brewer, M.T.; Thompson, R.C.; Moscatelli, D.; Presta, M.; Rifkin, D.B.

Biochem. Biophys. Res. Commun. 144, 543-550, 1987

A:Title: A form of human basic fibroblast growth factor with an extended amino termin

A:Reference number: S42242; MUID:87213238; PMID:3579930





Matches 147; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

[illegible]

## RESULT 11

basic fibroblast growth factor - sheep  
N:Alternate names: prostactropin  
O:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
P:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S00185  
R:Simpon, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, L.J.; Nice, E.C.; Rubira, M.R.; Burgess  
FEBS Lett. 224, 128-132, 1987  
A:Title: Primary structure of ovine pituitary basic fibroblast growth factor.  
A:Reference number: S00185; MUID:88055577; PMID:3678486  
A:Accession: S00185  
A:Molecule type: protein  
C:Residues: 1-146 <SIM>  
C:Superfamily: fibroblast growth factor  
C:Keywords: growth factor; heparin binding; mitogen  
F:18-22/Region: heparin binding #status predicted  
F:107-110/Region: heparin binding #status predicted

Query Match	31.98;	Score 764;	DB 1;	Length 146;
Best Local Similarly	97.38;	Pred. No. 8.3e+48;		
Matches 142;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

0y	287	PALEDEGSGAGFPBGHKDKDKRLYCKKNGGFFLRHPDGRVDGYREKSDPIKIQLOAEER	346
	1	PALEDEGSSSPFPBGHKDKDKRLYCKKNGGFFLRHPDGRVDGYREKSDPIKIQLOAEER	60
0y	347	GVASIKGCANRYLAMEDEBRLASKCVTGECEFFERLESNNYNTYRSRKYTSWYALKR	406
	61	GVASIKGCANRYLAMEDEBRLASKCVTGECEFFERLESNNYNTYRSRKYTSWYALKR	120
0y	407	TGOYKLGSKTGGOKALFLPMSAAS	432
	121	TGOYKLGSKTGGOKALFLPMSAAS	146

## RESULT 1.2

basic fibroblast growth factor - short-tailed opossum (*Monodelphis domestica*) (fragment).  
C:Species: *Monodelphis domestica*  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
C:Accession: S31622  
R:Rusewicz, D.F.; Sabourin, C.L.K.; Budge, C.L.; Ley, R.D.  
Submitted to the EMBL Data Library, September 1992  
A:Description: Characterization of cDNA encoding basic fibroblast growth factor of the m  
A:Reference number: S31622  
A:Accession: S31622  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-164 <KUS>  
A:Cross-references: EMBL:Z5154  
A:Superfamily: fibroblast growth factor

Query Match	31.5%	Score 754.5;	DB 2;	Length 164;
Best Local Similarity	92.3%	Pred. No. 4.7e-47;		
Matches 144;	Conservative	5;	Mismatches 6;	Indels 1;
				Gaps 1.

QY 278 MAAGSITLLPALPED-GGSGAFPFGHKDPKRLCYCKNGFFLRIHPDGRVDGVREKSDPH 336

```
Db      9 MAAGSITTLPALSGDGGGCAFPFGHFKDPKRLCYCKNGGFFLRIHPPDGRVDGIRESDPN 68
```

QY 337 IKLQDAEEGVSTKGVCANRYLAKMEDGRLLASKCVIDECFFERLESNNYNTYRSRK 396

Db 69 IKLQDAEEGVSTKGVCANRYLAKMEDGRLLAKKYVTECFEERLESNNYNTYRSRK 128

```
QY 397 YTSNVAALKRTGQYKLGSKTGPQKAILFLPMSAAS 432
    | : : | | | | | | | | | | | | | | | | | | |
Db 129 YSNMVAALKRTGQYKLGSKTGPQKAILFLPMSAKS 164
```

RESULT 13  
249934

basic fibroblast growth factor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999  
C:Accession: A48834; S23636  
R:Barja, A.Z.; Meljers, C.; Zeller, R.  
Dev. Biol. 157, 110-118, 1993  
A:Title: Expression of alternatively spliced bFGF first coding exons and antisense mRNA  
A:Reference number: A48834; MUID:93246053; PMID:7683281  
A:Accession: A48834  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-189 <BOR>  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIT:131000, NCBIT:131001)  
R:Miltrani, E.; Gruenbaum, Y.; Shohat, H.; Ziv, T.  
Development 109, 387-393, 1990  
A:Title: Fibroblast growth factor during mesoderm induction in the early chick embryo  
A:Reference number: S23636; MUID:90382254; PMID:2401202  
A:Accession: S23636  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 95-128 <MIT>  
A:Cross-references: EMBL:X56804; NID:962855; PIDD:CAA0139.1; PID:962856  
A:Superfamily: fibroblast growth factor

Query Match	31.4%	Score	753	DB 2:	Length	189
Best Local Similarity	91.6%	Pred. No.	7.3e-47			
Matches 141	Conservative	5	Mismatches	8	Indels	0
					Gaps	0

0y	279	AAGSITTLPALPEDEGSGAAPPGHFKPKPRLTYCNGNGEFLRIHDDGVVDVAKRESDPHK	338
Db	36	AAGSITTLPALPDGCGGAAFPFGHFKPKPRLTYCNGNGEFLRIHDDGVVDVAKRESDPHK	95
0y	339	LQLOAERGVSIGVCANRLAMKEDGRLLASCVTIDCEFFERLESNNYNTYRSKTYT	398
Db	96	LQLOAERGVSIGVCANRLAMKEDGRLLALCAAECECFERLESNNYNTYRSKYS	155

```
Oy      399 SWYVALKRTGQYYKIGSKTGPQAKILFLPMSAAS 4322
          |||||
Db      156 DWYVALKRTGQYKPCPKTGPGQAKILFLPMSAKS 1899
```

## RESULT 14

fibroblast growth factor - rabbit (fragment)  
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: I46711  
 R:Winkles, J.A.; Friesel, R.; Alberts, G.F.; Janat, M.F.; Liao, G.  
 Am. J. Pathol. 143, 518-527, 1993  
 A:Title: Elevated expression of basic fibroblast growth factor in an immortalized rat  
 A:Reference number: I46711; MUID:93343209; PMID:8342599  
 A:Accession: I46711  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-137 <MIN>  
 A:References: GB:I12034, NID:g165014, PIDN:AAA31248.1, PID:g165015  
 A:Superfamily: fibroblast growth factor

Query Match	30.8%	Score 738;	DB 2;	Length 137;
Best Local Similarity	99.3%	Pred. No. 5.5e-46;		
Matches 136; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;



GenCore version 5.1.4.p5\_4578  
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# OM protein - protein search, using sw model

Run on: March 13, 2003, 06:12:41 ; Search time 22 Seconds

(Without alignments)  
861.576 Million cell updates/sec

Title: US-09-775-964-5

Perfect score: 2398

Sequence: 1 PTDLRFTNIGDTRMTWAP.....LVTLPHPNLHGPELIDVPST 457

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

otal number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1474	61.5	2386	1	P02751 homo sapien
2	1396	58.2	2265	1	P07589 mus taurus
3	1345	56.1	2477	1	P04937 ratu
4	1340	55.9	2477	1	P11276 mus musculi
5	1210.5	50.5	1256	1	P11722 gallu
6	1051.5	43.8	1328	1	P091289 pleurodeles
7	1020.5	42.6	2481	1	Q91740 xenopus lae
8	820	34.2	155	1	P09038 homo sapien
9	811	33.8	155	1	P03699 bos taurus
10	805	33.6	155	1	P20003 ovis aries
11	792.5	33.0	154	1	P13109 ratu
12	777.5	32.4	154	1	P15655 mus musculi
13	754.5	31.5	156	1	P48798 monodelphis
14	753	31.4	158	1	P48800 gallu
15	738	30.8	137	1	P48799 cryotolagus
16	681	28.4	157	1	P12226 xenopus lae
17	425.5	17.7	155	1	P34004 mesocricetu
18	417.5	17.4	155	1	P19596 gallu
19	416.5	17.4	155	1	P05330 homo sapien
20	411.5	17.2	155	1	P01035 mus musculi
21	403.5	16.8	152	1	P20002 sus scrofa
22	400.5	16.7	155	1	P03668 bos taurus
23	354.5	14.8	3063	1	Q09715 homo sapien
24	345.5	14.4	3119	1	Q06047 mus musculi
25	339.5	14.2	639	1	Q28902 oryctolagus
26	338.5	14.1	1746	1	Q29116 sus scrofa
27	334.5	13.9	2201	1	P24821 homo sapien
28	333.5	13.9	929	1	Q91145 notophthalm
29	331	13.8	1808	1	P10039 gallu
30	309	12.9	522	1	Q28775 canis fami
31	309	12.9	3124	1	P13344 gallu
32	307	12.8	522	1	Q28377 equus cabal
33	290.5	12.1	1888	1	P32018 gallu

## ALIGNMENTS

RESULT 1	ID	SEQUENCE	STANDARD	PRT	AA
AC	P02751	Q14326			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).				
GN	FN1 OR FN.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
NC	NCBI_Taxid=9606;				
IN	[1]				
RP	SEQUENCE OF 1-38 FROM N.A.				
RX	MEDLINE=87030890; PubMed=3770189;				
RA	Gutman A., Yamada K.M., Kornblith A.R.;				
RT	"Human fibronectin is synthesized as a pre-propolypeptide.";				
RL	FEBS Lett. 207:145-148(1986).				
RN	[2]				
RP	SEQUENCE OF 1-49 FROM N.A.				
RX	MEDLINE=8717578; PubMed=3031656;				
RA	Dean D.C., Bowlin C.L., Bourgeois S.;				
RT	"Cloning and analysis of the promoter region of the human fibronectin gene.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).				
RN	[3]				
RP	SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.				
RX	MEDLINE=85284965; PubMed=2992939;				
RA	Kornblith A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;				
RT	"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";				
RL	EMBO J. 4:1755-1759(1985).				
RN	[4]				
RP	SEQUENCE OF 973-2081 AND 2113-2386 FROM N.A.				
RX	MEDLINE=84272258; PubMed=6462919;				
RA	Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;				
RT	"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";				
RL	Nucleic Acids Res. 12:5853-5868(1984).				
RN	[5]				
RP	SEQUENCE OF 1594-2386 FROM N.A.				
RX	MEDLINE=85280409; PubMed=2992573;				
RA	Bernard M.P., Kolbe M., Weil D., Chu M.-L.;				
RT	"Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";				
RL	Biochemistry 24:2698-2704(1985).				
RN	[6]				
RP	SEQUENCE OF 32-290.				
RX	MEDLINE=84032463; PubMed=6630202;				
RA	Garcia-Pardo A., Pearstein E., Frangione B.;				
RT	"Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";				
RL	J. Biol. Chem. 258:12670-12674(1983).				
RN	[7]				

34	283	11.8	4289	1	TENX_HUMAN	P22105 homo sapien
35	272	11.3	2944	1	CA17_HUMAN	O02388 homo sapien
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37	266	11.1	194	1	FGF4_CHICK	P48804 gallu
38	264	11.0	220	1	FGF3_CHICK	P48801 gallu
39	258.5	10.8	206	1	FGF4_BOVIN	P48803 bos taurus
40	257.5	10.7	266	1	FGF5_RAT	P48807 ratu
41	256.5	10.7	264	1	FGF5_MOUSE	P15656 mus musculi
42	255.5	10.7	256	1	FGF3_BRARE	P48802 brachydanio
43	251.5	10.5	268	1	FGF5_HUMAN	P12034 homo sapien
44	250	10.4	208	1	FGF6_MOUSE	P21658 mus musculi
45	249	10.4	208	1	FGF6_HUMAN	P10767 homo sapien

RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.  
RA MEDLINE-87080265; PubMed-3024962;  
RT Owens R.J., Baralle F.E.;  
RT "Mapping the collagen-binding site of human fibronectin by expression  
RT in *Escherichia coli*.";  
RL EMBO J. 5:2825-2830(1986).  
RN [8]  
RP SEQUENCE OF 1441-1548.  
RX MEDLINE-82265604; PubMed-7050098;  
RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;  
RT "The cell attachment domain of fibronectin. Determination of the  
RT primary structure.";  
RL J. Biol. Chem. 257:9593-9597(1982).  
RN [9]  
RP SEQUENCE OF 1434-1537 FROM N.A.  
RX MEDLINE-83390929; PubMed-6688418;  
RA Oldberg A., Linney E., Ruoslahti E.;  
RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for  
RT the cell attachment domain in human fibronectin.";  
RL J. Biol. Chem. 258:10193-10196(1983).  
RN [10]  
RP SEQUENCE OF 1448-1540 FROM N.A.  
RX MEDLINE-86111901; PubMed-3003095;  
RA Oldberg A., Ruoslahti E.;  
RT "Evolution of the fibronectin gene. Exon structure of cell attachment  
RT domain.";  
RL J. Biol. Chem. 261:2113-2116(1986).  
RN [11]  
RP SEQUENCE OF 1712-1739 FROM N.A.  
RX MEDLINE-87026578; PubMed-3021206;  
RA Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.;  
RT "Human liver fibronectin complementary DNAs: identification of two  
RT different messenger RNAs possibly encoding the alpha and beta  
RT subunits of plasma fibronectin.";  
RL Biochemistry 25:4936-4941(1986).  
RN [12]  
RP SULFATION.  
RX MEDLINE-86042625; PubMed-2414772;  
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;  
RT "Tyrosine sulfation of proteins from the human hepatoma cell line  
RT HepG2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).  
RN [13]  
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.  
RX MEDLINE-95081153; PubMed-798369;  
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;  
RT "Further characterization of the NH2-terminal fibrin-binding site on  
RT fibronectin.";  
RL J. Biol. Chem. 269:31938-31945(1994).  
RN [14]  
RP STRUCTURE BY NMR OF 32-92.  
RX MEDLINE-96069779; PubMed-758366;  
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;  
RT "High-resolution structural studies of the factor XIIIa crosslinking  
RT site and the first type I module of fibronectin.";  
RL Nat. Struct. Biol. 2:946-950(1995).  
RN [15]  
RP STRUCTURE BY NMR OF 182-275.  
RX MEDLINE-94141923; PubMed-8308892;  
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,  
RT Campbell I.D.;  
RT "Solution structure of a pair of fibronectin type I modules with  
RT fibrin binding activity.";  
RL J. Mol. Biol. 235:1302-1311(1994).  
RN [16]  
RP STRUCTURE BY NMR OF 406-464.  
RX MEDLINE-96179558; PubMed-9514732;  
RA Sligh H., Pickford A.R., Potts J.R., Campbell I.D.;  
RT "Solution structure of the glycosylated second type 2 module of  
RT fibronectin.";  
RL J. Mol. Biol. 276:177-187(1998).  
RN [17]  
RP STRUCTURE BY NMR OF 1447-1540.

RX MEDLINE-93046665; PubMed-1423622;  
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;  
RT "The three-dimensional structure of the tenth type III module of  
RT fibronectin: an insight into RGD-mediated interactions.";  
RL Cell 71:671-678(1992).  
RN [18]  
RP STRUCTURE BY NMR OF 1447-1540.  
RX MEDLINE-92162710; PubMed-1311202;  
RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,  
RT Campbell I.D.;  
RT "III module assignment and secondary structure of the cell adhesion type  
RT III module of fibronectin.";  
RL Biochemistry 31:2068-2073(1992).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1535.  
RX MEDLINE-94166075; PubMed-8120888;  
RA Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xuong N.-H.,  
RT Ruoslahti E., Ely K.R.;  
RT "Crystal structure of the tenth type III cell adhesion module of  
RT human fibronectin.";  
RL J. Mol. Biol. 236:1079-1092(1994).  
RN [20]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.  
RX MEDLINE-99177162; PubMed-10075919;  
RA Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.I.;  
RT "Crystal structure of a heparin- and integrin-binding segment of human  
RT fibronectin.";  
RL EMBO J. 18:1468-1479(1999).  
RN [21]  
RP FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND  
HEALING, AND MAINTENANCE OF CELL SHAPE.  
-!- SUBUNIT, MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
-!- VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;  
-!- TO A LESSER EXTENT HOMODIMERS.  
-!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" AND THE CONNECTING  
-!- STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN  
-!- OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.  
-!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE ALTERNATIVE FORM) IS SECRETED  
-!- BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC  
-!- FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
-!- DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
-!- PTM: SULFATED.  
-!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.  
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.  
-!- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III DOMAINS.  
-!- THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
-!- between the Swiss Institute of Bioinformatics and the EMBL outstation -  
-!- the European Bioinformatics Institute. There are no restrictions on its  
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-!- or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch))  
-!- -----  
DR EMBL: M15801; AAA53376.1; -  
DR EMBL: X02761; CAA26536.1; -  
DR EMBL: M10905; AAA52462.1; -  
DR EMBL: M12549; AAA58483.1; -  
DR EMBL: M14059; AAA52463.1; -  
DR PIR: A26460; FNH0.  
DR PDB: 1TF7; 31-JAN-94.  
DR PDB: 1TTG; 31-JAN-94.  
DR PDB: 1TNA; 30-APR-94.  
DR PDB: 1TNE; 29-JAN-96.  
DR PDB: 1TFR; 15-OCT-95.  
DR PDB: 1FNH; 16-MAR-99.  
DR PDB: 2FN2; 16-SEP-98.  
DR GlycoSuiteDB: P02751; -  
DR GeneW: HGNC:3778; FN1.  
DR MIM: 135600; -  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR003961; FN\_III.

Query Match 61.5%; Score 1474; DB 1; Length 2386;  
 Best Local Similarity 46.8%; Pred. No. 6.5e-98;  
 Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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OY 1 PTDLFTNIGPDMRYMVAAPPSIDLTNLFVRSVPYKNEDEVAELISPSDNAVLTNLL 60
DB 1270 PDLRTNIGPDMRYMVAAPPSIDLTNLFVRSVPYKNEDEVAELISPSDNAVLTNLL 1329
OY 61 PTEVEVSVSSVYEQHESTPLGRKGTGIDSDPTGIDFSITANSFTVHIAIPRATTGTR 120
DB 1330 PTEVEVSVSSVYEQHESTPLGRKGTGIDSDPTGIDFSITANSFTVHIAIPRATTGTR 1389
OY 121 IHHHEHESGPREDRVPVSRNSITLTNLTPEEYVSVIALNGRSPESLLIGQOSTVD 180
DB 1390 IHHHEHESGPREDRVPVSRNSITLTNLTPEEYVSVIALNGRSPESLLIGQOSTVD 1449
OY 181 VPRDEVVAATPTSLISMDAPAVTVRYRYRITYGETGNSPVQETVPKSKSTATISGLK 240
DB 1450 VPRDEVVAATPTSLISMDAPAVTVRYRYRITYGETGNSPVQETVPKSKSTATISGLK 1509
OY 241 PEVDYTIYVATGAGDSASSKPSISINRTFIDKPS-----M 278
DB 1510 PEVDYTIYVATGAGDSASSKPSISINRTFIDKPSQMVTVDVQDINSISVKMLPSSSEV 1569
OY 279 AAGSTITL----- 287
DB 1570 TGYRVTTTPKNGPPTKTKTACPDQTEMTIEGLQPTVEVSVYAONPGESOPLVQTVAV 1629
OY 288 -----ALPEDGSGAFP-PGHFKDPKRL 309
DB 1630 TNIDRPKGLAFTDVVDYSIKIMESPQGVSRVRYTSPEQIHLEFPAPGEEDTAEL 1689
OY 310 YKNGG-----FELRH-----PDGRV 326
DB 1690 OGIRPGESEVTVSVALHDMESOPLTGSTAIPAPTDLKTQVPTSLSAOWTPPNVOL 1749
OY 327 DGVK-----EKSDPHIKLOLAEEGVYSIKGVCANRY-----LAMEKEDGLASK----- 372
DB 1750 TGYRVATVPKKEKTPKKEINLAPDSSVYSGLMATKIEVSYALKD-----TLTSKPAOG 1806
OY 373 -----CVTDEC-----FFERLESNNYTYRS-----R 395
DB 1807 VVTTLENVSPRRARVTDATETTTITSMRTKETITGFGVDAPVANGQPIQITIKPDVR 1866
OY 396 KTY-----SWYVA 403
DB 1867 SYTTTGLQGTDKYIYLTLDNARSSPVVIDASTAIDAPSNLRLATTPNSLLVSWOPR 1926
OY 404 LKRTGQY-----KLSK-----TG--PGOKAILFL-----PM- 428
DB 1927 RARITCYIIKIYKPEGSPREVPVRRPRGVTEATITISLEGTETIIVIALKNOKSEPLI 1986
OY 429 -SAASDELQVLTLPHPNLHGPPEILDVPS 457
DB 1987 GRKKTDELQVLTLPHPNLHGPPEILDVPS 2016

RESULT 2
FINC_BOVIN STANDARD: PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibronectin (FN).
GN FN1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Soltrop-Jensens L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
RT of internal homology.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
RT fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -!- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES, CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS) MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -!- PTM: SULFATED (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -!- SIMILARITY: CONTAINS 15 FIBRONECTIN TYPE III DOMAINS.
CC
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CC
CC EMBL; K00800; AAA30521.2; -
CC PIR; A26452; FNBO.
CC HSSP; P02751; 2FN2.
CC
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR000562; FN_Type_II.
CC InterPro: IPR000083; Fibnrcn1.
CC InterPro: IPR003962; FNIII_repeat.
CC Pfam; PF00039; fn1; 12.
CC Pfam; PF00040; fn2; 2.
CC Pfam; PF00041; fn3; 15.
CC PRINTS; PR00012; ENTPEI.
CC PRINTS; PR00013; ENTPEI1.
CC PRINTS; PR00014; ENTPEI11.
CC ProDom; PD000995; FN_Type_II; 2.
CC SMART; SM00058; FN1; 12.
CC SMART; SM00059; FN2; 2.
CC SMART; SM00060; FN3; 14.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS00023; FIBRONECTIN_2; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 12.
CC GlycoProtEx: Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing.
CC MOD_RES 1 241 PYRROLIDONE CARBOXYLIC ACID.
CC FT 21 241 FIBRIN- AND HEPARIN-BINDING 1.
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 FIBRIN-BINDING 2.  
 FIBRONECTIN TYPE-I 1.  
 FIBRONECTIN TYPE-I 1.  
 FIBRONECTIN TYPE-I 2.  
 FIBRONECTIN TYPE-I 3.  
 FIBRONECTIN TYPE-I 4.  
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 FIBRONECTIN TYPE-I 6.  
 FIBRONECTIN TYPE-II 1.  
 FIBRONECTIN TYPE-II 2.  
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 FIBRONECTIN TYPE-I 9.  
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 FIBRONECTIN TYPE-III 4.  
 FIBRONECTIN TYPE-III 5.  
 FIBRONECTIN TYPE-III 6.  
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 FIBRONECTIN TYPE-III 9.  
 FIBRONECTIN TYPE-III 10.  
 FIBRONECTIN TYPE-III 11.  
 FIBRONECTIN TYPE-III 12.  
 FIBRONECTIN TYPE-III 13.  
 FIBRONECTIN TYPE-III 14.  
 CONNECTING STRAND 3 (CS-3) (V REGION).  
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 FIBRONECTIN TYPE-I 11.  
 FIBRONECTIN TYPE-I 12.  
 CELL ATTACHMENT SITE.

FT CARBOHYD 1987 1987 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 1943 1943 O-LINKED (GALNAC. . .).  
 FT CARBOHYD 1944 1944 O-LINKED (GALNAC. . .).  
 FT MOD\_RES 2263 2263 PHOSPHORYLATION.  
 SQ SEQUENCE 2265 AA; 249557 MW; C2D2IDA86F98D5C CRC64;  
 Query Match 58.2%; Score 1396; DB 1; Length 2265;  
 Best Local Similarity 48.6%; Pred. No. 2,5e+92;  
 Matches 327; Conservative 38; Mismatches 76; Indels 232; Gaps 17;  
 QY 1 PMDLPTNIGPTMTVATNPAPPSIDLTNLTLYSSVKNEEDVAELISPSDNAVITNL 60  
 DB 1239 PDLRTNAGPTMTVATNPAPPSIELTNLTLYSSVKNEEDVAELISPSDNAVITNL 1298  
 QY 61 PGTETVVSYSVYEOHESTPLRGKRTGLDPTGIDFSDITANSFTVMHAPRATITGTR 120  
 DB 1299 PGTETVVSYSVYEOHESTPLRGKRTGLDPTGIDFSDITANSFTVMHAPRATITGTR 1358  
 QY 121 IHHHEHESGPREDRVPHSRNSITLTNLTPTETEVVSIVALNGREESPLIGQOSTVSD 180  
 DB 1359 IHHHEHESGPREDRVPHSRNSITLTNLTPTETEVVSIVALNGREESPLIGQOSTVSD 1418  
 QY 181 VPRDELVAVATPTSLISMDAPAVTVRYRITTYGETGNSPQOETVPGSKSTATISGLK 240  
 DB 1419 VPRDELVAVATPTSLISMDAPAVTVRYRITTYGETGNSPQOETVPGSKSTATISGLK 1478  
 QY 241 PGVDVITTYAVATGSDSPASSKPSISINRTETIDPMSA-----AGSITLPA---- 288  
 DB 1479 PGVDVITTYAVATGSDSPASSKPSISINRTETIDPMSA-----AGSITLPA---- 1538  
 QY 289 -----LPEDGSCAFPPGHEKDK-----RXYCKN----- 313  
 DB 1539 TGYRTYTPAKNG-----PGPSKTKVGPDTENTIEGLPTVEYVSVAQONGBESP 1592  
 QY 314 -----GFFLIHPDGKVDGVRKESDPHI 337  
 DB 1593 LVQVATTPAPNLKFTQVTPTSLSLAQMTAPNVOLTGIRAVTP-----KERTGPK 1645  
 QY 338 KLOLAERGVSISGVCANRY---LANKEDGRLLASK-----CVT 375  
 DB 1646 EINLAPDSSSVVSGLMVATKYEVSYALKD---TLTSHPAGGVTTLENSPPRRARYT 1702  
 QY 376 DEC-----FFERLESNNY-----NTYRSRK 396  
 DB 1703 DATETTITISMRKTETITGFQVDAIPANGQPTQRTIRPDVRSYITGLOPCTDKIHL 1762  
 QY 397 YT-----SMYVALKRTGY-----KLGSK 415  
 DB 1763 YTLNDNARSSPVVIDASTAIDAPSNLRLATTPNSILVSWOPRRARITGYIIRKEKPCSP 1822  
 QY 416 -----TG--PGOK---ALFLPMSAAS-----DELQVLTLPHP 444  
 DB 1823 PREVPAPRPVTEATITGLEGTETTYIVALKNNOKSEPLIGRKKIDELQVLTLPHP 1882  
 QY 445 NLHGPEILDVPEST 457  
 DB 1883 NLHGPEILDVPEST 1895  
 RESULT 3  
 FINE\_RAT STANDARD: PRT: 2477 AA.  
 AC P04937;  
 DT 13-AUG-1987 (rel. 05, Created)  
 DT 01-NOV-1990 (rel. 16, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Fibronectin precursor (FN).  
 GN FNI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]



FT DISULFID 561 589 BY SIMILARITY.  
 FT DISULFID 587 599 BY SIMILARITY.  
 FT DISULFID 2296 2325 BY SIMILARITY.  
 FT DISULFID 2323 2335 BY SIMILARITY.  
 FT DISULFID 2341 2368 BY SIMILARITY.  
 FT DISULFID 2366 2378 BY SIMILARITY.  
 FT DISULFID 2385 2409 BY SIMILARITY.  
 FT DISULFID 2407 2423 BY SIMILARITY.  
 FT DISULFID 2458 2458 INTERCHAIN (WITH 2462 OF OTHER CHAIN).  
 FT DISULFID 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN).  
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1290 1290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2198 2198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MOD\_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPLIC 1720 1809 MISSING (IN ISOFORM FNII-13 LESS).  
 FT VARSPLIC 2082 2106 MISSING (IN ISOFORM LAMBDA-RLF4-5).  
 FT VARSPLIC 2082 2200 MISSING (IN ISOFORM LAMBDA-RLF6).  
 FT CONFLICT 2318 2318 G -> A (IN REF. 3).  
 SQ SEQUENCE 2477 AA; 272510 MW; B4391A472CEDEB5 CRC64;

Query Match 56.1%; Score 1345; DB 1; Length 2477;  
 Best Local Similarity 42.4%; Pred. No. 1.3e-88;  
 Matches 318; Conservative 49; Mismatches 87; Indels 296; Gaps 18;

1 PTDLRTNIGPDPMRYTWPAPPSIDLTNPLRYSPKNEEDVAELSTSPDNVVLTLNL 60  
 1360 PTDLRTNIGPDPMRYTWPAPPSIDLTNPLRYSPKNEEDVAELSTSPDNVVLTLNL 1419  
 61 PGEVYVSVSYEHOESTPLRGOKTGLDPSGIDPSDTANSFYHMAAPATITGR 120  
 1420 PGEVYVSVSYEHOESTPLRGOKTGLDPSGIDPSDTANSFYHMAAPATITGR 1479  
 121 IRHHPFSGRPREDRYPHSRNSITLTNLTGFEYVSVYALNGREBSPLLICQOSTVD 180  
 1480 IRHHAESARPRDPRPSPRNSITLTNLTGFEYVSVYALNGREBSPLLICQOSTVD 1539  
 181 VPRDLEVVAATPTSLISMDAPAVYRYRITGETGNSPVQEFYVPGSKSTATISGLK 240  
 1540 VPRDLEVIASTPTSLISMDAPAVYRYRITGETGNSPVQEFYVPGSKSTATISGLK 1599  
 241 PGVDYTTVAVNGRSDSPASSKPSISNRTETDKPS-----M 278  
 1600 PGADYTTTLYAVNGRSDSPASSKPSISNRTETDKPSOMQVTDVODNSISVRLPSTSPV 1659  
 279 AAGSITLTP----- 287  
 1660 TGYRVTTAPKNGLGPKRSQVSPDQTEMTIEGLPVEYVSVYQNRNGESQPLVQTAV 1719  
 288 -----ALPEDGSSGAF-P-GHFKPKPKRL 309  
 1720 TNIDRPKGLAFDVIDVDSIKIAMESPOGVSRVRYTSSPEDITHELFPAPDDEDTAEL 1779  
 310 Y-----CKNGF-----FLKIH-----EDGRV 326  
 1780 HGLRPGSEYVSVYALNGREBSPGLGVOSTAIPAPNLTQSPPTTLTAQMTAIVSVKL 1839  
 327 DGYR-----EKSDPHIKLOLAEBRGVSVIKVCANRY---LAKEDRGLASK--- 372  
 1840 TGYRVVTPREKTKPMKEINLSPDSTSVISGLMAYKRVSVYALKD---TLTSRAOG 1896  
 373 -----CVTDEC-----FFERLESNNY----- 389  
 1897 VVTLLENVSPRRARVYDATTETITISWRTETITGFQVDAIPANQOFPVORTISPDVR 1956  
 390 -----NTYRSRYT-----SWYVA 403  
 1957 SYTITGLQPTDYKIHLYTLINDNARSSPVVIASTADAPSNLRPLTTTPNSLLVSWQAP 2016

OY 404 LKRTGOY-----KLGSK-----TG--PGOKAILFL-----PW- 428  
 DB 2017 RARITGYIIKYEKPSPREVPRPRPVTEATITGLERGTEYTYIVALKNNKSEPLI 2076  
 OY 429 -SASDELPOVLTLPHPNLHGPEILDVPT 457  
 DB 2077 GRKKTDELPOVLTLPHPNLHGPEILDVPT 2106

## RESULT 4

FINE\_MOUSE STANDARD: PRT: 2477 AA.  
 AC P11276; Q61568; Q61567; Q64233;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibronectin precursor (FN) (Fragments).  
 GN FNI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE OF 1-28 FROM N.A.  
 RC TISSUE=Liver;  
 RA POLLY P., Nicholson R.C.;  
 RT "Sequence of the mouse fibronectin-encoding gene promoter region.";  
 RL gene 137:353-354(1993).  
 RN [2]  
 RP SEQUENCE OF 562-834 FROM N.A.  
 RC STRAIN=NMRI.  
 RA TATES J.F., Weller A., Timpi R., Ekblom M., Ekblom P.;  
 RT Regulation of mesenchymal extracellular matrix protein synthesis by  
 RT transforming growth factor-beta and glucocorticoids in tumor  
 RT stroma.";  
 RL J. Cell Sci. 108:2153-2162(1995).  
 RN [3]  
 RP SEQUENCE OF 899-2376 FROM N.A.  
 RA GORSKI G., Aros M., Norton P.;  
 RT Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 2375-2477 FROM N.A.  
 RA MEDLINE=88124587; PubMed=3124113;  
 RT "Induction of fibronectin gene transcription and mRNA is a primary  
 RT response to growth-factor stimulation of AKR-2B cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).  
 RN [5]  
 RP SEQUENCE OF 2375-2477 FROM N.A.  
 RC TISSUE=Kidney;  
 RA MEDLINE=93011702; PubMed=1327855;  
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-  
 RT infected mouse kidney cells.";  
 RL Exp. Cell Res. 202:464-470(1992).  
 RN [6]  
 RP STRUCTURE BY NMR OF 1447-1630.  
 RA MEDLINE=98202578; PubMed=9533887;  
 RA COPLE V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,  
 RA Pastor R.W., Krueger S., Torchia D.A.;  
 RT "Solution structure and dynamics of linked cell attachment modules of  
 RT mouse fibronectin containing the RGD and synergy regions: comparison  
 RT with the human fibronectin crystal structure.";  
 RL J. Mol. Biol. 277:663-682(1998).  
 CC -I- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND  
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -I- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
 CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS.  
 CC TO A LESSER EXTEND HOMODIMERS.

CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.

CC -!- PTM: SULFATED (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.

CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.

CC -!- SIMILARITY: CONTAINS 17 FIBRONECTIN TYPE III DOMAINS.

CC -----

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CC -----

DR EMBL: 222729; CAA80422.1; -

DR EMBL: X82402; CAA57796.1; -

DR EMBL: X93167; CAA63654.1; -

DR EMBL: M18194; AAA37636.1; -

DR EMBL: S45680; AAB33491.1; -

DR PIR: A31371; A31371.

DR PIR: C60597; C60597.

DR PDB: IMEN; 29-APR-98.

DR PDB: 2MFN; 29-APR-98.

DR MGD: MGI:95566; Fnl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR003961; FN\_III.

DR InterPro: IPR000562; FN\_Type\_II.

DR InterPro: IPR000083; Flnrcnt1.

DR Pfam: PF00039; fnl; 4.

DR Pfam: PF00041; fn3; 17.

DR PRINTS: PR00014; ENTPEP11.

DR SMART: SM00058; FNI; 4.

DR SMART: SM00060; FN3; 14.

DR PROSITE: PS00022; EGF\_1; 1.

DR PROSITE: PS00023; FIBRONECTIN\_2; PARTIAL.

DR PROSITE: PS01253; FIBRONECTIN\_1; 4.

DR GlycoProtein: Plasma: Heparin-binding; Acute phase: Phosphorylation; Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal;

KM 3D structure.

KM 1 SIGNAL 32

FT CHAIN 33 2477 FIBRONECTIN.

FT DOMAIN 53 273 FIBRIN- AND HEPARIN-BINDING 1.

FT DNA\_BIND 308 608 COLLAGEN-BINDING.

FT 1357 1630 CELL-ATTACHMENT.

FT DOMAIN 1811 2081 HEPARIN-BINDING 2.

FT 2296 2427 HEPARIN-BINDING 2.

FT 51 96 FIBRONECTIN TYPE-I 1.

FT DOMAIN 96 140 FIBRONECTIN TYPE-I 2.

FT 185 185 FIBRONECTIN TYPE-I 3.

FT DOMAIN 185 230 FIBRONECTIN TYPE-I 4.

FT 230 272 FIBRONECTIN TYPE-I 5.

FT DOMAIN 306 343 FIBRONECTIN TYPE-II 1.

FT 345 404 FIBRONECTIN TYPE-II 1.

FT 469 469 FIBRONECTIN TYPE-II 2.

FT 468 516 FIBRONECTIN TYPE-I 7.

FT 516 559 FIBRONECTIN TYPE-I 8.

FT 559 602 FIBRONECTIN TYPE-I 9.

FT 602 706 FIBRONECTIN TYPE-I 1.

FT 706 808 FIBRONECTIN TYPE-II 2.

FT 808 903 FIBRONECTIN TYPE-III 3.

FT 904 994 FIBRONECTIN TYPE-III 4.

FT 995 1084 FIBRONECTIN TYPE-III 5.

FT 1085 1172 FIBRONECTIN TYPE-III 6.

FT 1172 1264 FIBRONECTIN TYPE-III 7.

FT 1265 1355 FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN 1).

FT DOMAIN 1356 1446 FIBRONECTIN TYPE-III 9.

FT DOMAIN 1447 1536 FIBRONECTIN TYPE-III 10.

FT 1537 1630 FIBRONECTIN TYPE-III 11.

FT 1631 1720 FIBRONECTIN TYPE-III 12.

FT 1721 1810 FIBRONECTIN TYPE-III 13.

FT 1811 1902 FIBRONECTIN TYPE-III 14.

FT 1903 1991 FIBRONECTIN TYPE-III 15.

FT 1992 2081 FIBRONECTIN TYPE-III 16.

FT 2082 2201 CONNECTING STRAND 3 (CS-3) (V REGION).

FT 2202 2283 FIBRONECTIN TYPE-III 17.

FT 2284 2338 FIBRONECTIN TYPE-I 10.

FT 2339 2381 FIBRONECTIN TYPE-I 11.

FT 2383 2426 FIBRONECTIN TYPE-I 12.

FT 2426 2458 CELL ATTACHMENT SITE.

FT SITE 1614 1616 CELL ATTACHMENT SITE.

FT SITE 2181 2183 CELL ATTACHMENT SITE.

FT DISULFID 561 589 BY SIMILARITY.

FT DISULFID 587 599 BY SIMILARITY.

FT DISULFID 2296 2325 BY SIMILARITY.

FT DISULFID 2323 2335 BY SIMILARITY.

FT DISULFID 2341 2368 BY SIMILARITY.

FT DISULFID 2366 2378 BY SIMILARITY.

FT DISULFID 2385 2409 BY SIMILARITY.

FT DISULFID 2407 2423 BY SIMILARITY.

FT DISULFID 2458 2458 INTERCHAIN (WITH 2462 OF OTHER CHAIN).

FT DISULFID 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN).

FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1290 1290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2198 2198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MOD\_RES 2475 2475 PHOSPHORYLATION. (BY SIMILARITY).

FT CONFLICT 2440 2440 N -> T (IN REF. 5).

SO SEQUENCE 2477 AA; 271416 MW; 8D2B63B474E2A2M4 CMC64;

Query Match 55.9%; Score 1340; DB 1; Length 2477;

Best Local Similarity 41.7%; Pred. No. 3; le-88;

Matches 316; Conservative 46; Mismatches 85; Indels 310; Gaps 16;

QY 1 PTDLRFTNIGPDIMRVWAPPPSTDLNPLVRSVPVNEEDVLELSTSPSDNAVLTNLL 60

DB 1360 PTDLRFTNIGPDIMRVWAPPPSTDLNPLVRSVPVNEEDVLELSTSPSDNAVLTNLL 1419

QY 61 PGTREYVSVSVYEOHESFPLRGOKTGLDPSGTGIDSDTANSFYVHWIAPRATTGYR 120

DB 1420 PGTREYVSVSVYEOHESFPLRGOKTGLDPSGTGIDSDTANSFYVHWIAPRATTGYR 1479

QY 121 IRIHPEHFSRPRDRPHSRNSTLTNLTPGTREYVSVYALNGRESPLLIQGOQTVSD 180

DB 1480 IRIHPEHFSRPRDRPHSRNSTLTNLTPGTREYVSVYALNGRESPLLIQGOQTVSD 1539

QY 181 VPRDLFVAVATPTSLISMTAPAVTVRYRTTGTGSGNSPVQEFVPGSKSTATISGLK 240

DB 1540 VPRDLFVAVATPTSLISMTAPAVTVRYRTTGTGSGNSPVQEFVPGSKSTATISGLK 1559

QY 241 PGVDYTTVAVAVGRGDSPPASSKRPISINRYTEIDKPS-----M 278

DB 1600 PGADYTTTLAVAVGRGDSPPASSKRPISINRYTEIDKPSQOMQVTDVQDMSISVRMLPSTSPV 1659

QY 279 AAGSTITLP----- 287

DB 1660 TGYRVTTTPKNGLGPSKTKTASPQDEMTLEGLOPVEYVSVYAQNNGESOPLYOTAV 1719

QY 288 -----ALPEDGSGAFPPGHFD----- 305

DB 1720 TNDIPRKGAFITDVVDVDSIKIAMESPOGOVSRTKRVYTSSEPDGIRELPAPDGEDDTAEL 1779

QY 306 -----PKRLVCKN----- 313

DB 1780 QGLRPGSEYTVSVVALHDDMESQPLIGTQSPALPAPNTMLKLSQYTPSTFAQWIAPSVQL 1839

QY 314 GGFPLRIHPGRVDGVKEKSDPHIKILOAEERGVYSIKGVCANRY---LAKKEDGRLL 369

DB 1840 TGYRAVRVNP-----KEKGPMEKINLSPDSSSVIVSGIMVATKVEYVSVALKD---TL 1889

QY 370 ASK-----CVTDEC-----FFERLESNNY----- 389  
 DB 1890 TSPRAGVITTELENSPPRRARVDTATEETITISMTKETITITGQVDAIPANGOTPVOR 1949  
 QY 390 -----NTRYRSRKYT----- 398  
 DB 1950 SISPDVRSYITIGLOPGTDYKILHVLTLNDNARSSPYIIDASTAIDAPNSLRELTTPNSL 2009  
 QY 399 --SWVVALKRTGQY-----KLGSK-----TG--PGKAIILFL----- 426  
 DB 2010 LYSWQAPRARTIGYIIIRKPKSPREVPYRPRPGTEATITIGLEGTETIYIYALKRN 2069  
 QY 427 ----PW--SAASDELPOLYTLPHNHLGPEIILDPST 457  
 DB 2070 OKSEPLIGKRKTDLPOLVTLPHNHLGPEIILDPST 2106

## RESULT 5

FINC\_CHICK STANDARD: PRT: 1256 AA.

01-OCT-1989 (Rel. 12, Created)  
 01-NOV-1997 (Rel. 35, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fibronectin (FN) (Fragments).  
 GN FN1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE OF 1-50 FROM N.A.  
 RX MEDLINE=83117850; PubMed=6572007;  
 RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,  
 RT "Isolation of genomic DNA clones spanning the entire fibronectin  
 gene." Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).  
 RL [2]  
 RM SEQUENCE OF 51-1256 FROM N.A.  
 RC STRAIN=White Leghorn;  
 RA Norton P.A.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 227-415 FROM N.A.  
 RX MEDLINE=96183658; PubMed=8603103;  
 RA Gehris A.L., Brandli D.W., Lewis S.D., Bennett V.D.;  
 RT "The exon encoding the fibronectin type III-9 repeat is  
 constitutively included in the mRNA from chick limb mesenchyme and  
 cartilage." J. Biol. Chem. 268:1111-1115(1993).  
 RL [4]  
 RM Biochim. Biophys. Acta 1311:5-12(1996).  
 RN [5]  
 RP SEQUENCE OF 327-599 FROM N.A.  
 RX MEDLINE=88050950; PubMed=2823899;  
 RA Kubomura S., Ohara M., Karasaki Y., Taniguchi H., Gotch S.,  
 RT "Genetic analysis of the cell binding domain region of the chicken  
 fibronectin gene." J. Biol. Chem. 268:1111-1115(1993).  
 RL Biochim. Biophys. Acta 910:171-181(1987).  
 RN [6]  
 RP SEQUENCE OF 413-1256 FROM N.A.  
 RX MEDLINE=88142820; PubMed=2830487;  
 RA Norton P.A., Hynes R.O.;  
 RT "Alternative splicing of chicken fibronectin in embryos and in normal  
 and transformed cells." J. Biol. Chem. 268:1111-1115(1993).  
 RL Mol. Cell. Biol. 7:4297-4307(1987).  
 CC -I- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND  
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -I- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
 CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS.

CC TO A LESSER EXTEND HOMODIMERS.  
 CC -I- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING  
 CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN  
 CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.  
 CC -I- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED  
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC  
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 CC -I- P.W. SULFATED (BY SIMILARITY)  
 CC -I- SIMILARITY: CONTAINS AT LEAST 2 FIBRONECTIN TYPE I DOMAINS.  
 CC -I- SIMILARITY: CONTAINS AT LEAST 8 FIBRONECTIN TYPE III DOMAINS.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: V00432; CAA23714.1; -  
 CC EMBL: U21327; AAA73566.1; -  
 CC EMBL: X06533; CAA29781.1; -  
 CC EMBL: M26186; AAA48772.1; ALT\_SEQ.  
 CC EMBL: U20386; AAB01062.1; -  
 CC PIR: A28512; A28512.  
 CC PIR: A29355; A29355.  
 CC HSSP: P02751; 1FNH.  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR000562; FN\_Type\_II.  
 CC InterPro: IPR000083; FibrnctnI.  
 CC InterPro: IPR003962; FnIII\_repeat.  
 CC PRINTS: PR00014; FNTYPEIII.  
 CC SMART: SM00058; FN1\_3.  
 CC SMART: SM00060; FN3\_10.  
 CC PROSITE: PS00023; FIBRONECTIN\_2; PARTIAL.  
 CC PROSITE: PS01253; FIBRONECTIN\_1; 2.  
 CC KMW Glycoprotein; Plasma Heparin-binding; Acute phase; Cell adhesion;  
 CC Repeat; Sulfation; Alternative splicing.  
 CC FT NON\_TER 1 1  
 CC FT 50 51  
 CC FT 236 509  
 CC FT 690 961  
 CC FT 1153 1226  
 CC FT 327 415  
 CC FT 416 509  
 CC FT 510 599  
 CC FT 600 689  
 CC FT 690 781  
 CC FT 782 871  
 CC FT 872 961  
 CC FT 962 1082  
 CC FT 1083 1152  
 CC FT 1174 1218  
 CC FT 1219 1256  
 CC FT 493 495  
 CC FT 1176 1205  
 CC FT DISULFID 1203 1245  
 CC FT DISULFID 1221 1248  
 CC FT CARBOHYD 1078 1078  
 CC FT CONFLICT 516 516  
 CC FT 569 572  
 CC FT NON\_TER 1256 1256  
 CC SQ SEQUENCE 1256 AA; 137435 MW; 345A4CA0EAD71D9B CRC64;  
 CC Query Match 50.5%; Score 1210.5; DB 1; Length 1256;  
 CC Best Local Similarity 76.3%; Pred. No. 2.5e-79;  
 CC Matches 238; Conservative 23; Mismatches 32; Indels 19; Gaps 2;  
 CC 1 PDLARTNIGPMRTYMWPPSIDLNFVLRSPVKNEEDVAELISPSDNAVVTNLL 60  
 CC 239 PDLARTNIGPMRTYMWPPSIDLNFVLRSPVKNEEDVAELISPSDNAVVTNLL 298



DR EMBL: X66813; CAA47292.1; -.  
DR HSSP: P02751; IPNH.  
DR InterPro: IPRO00561; EGF-like.  
DR InterPro: IPRO03961; FN\_III.  
DR InterPro: IPRO00883; Fibrinctn1.  
DR Pfam: PF00039; fn1; 3.  
DR Pfam: PF00041; fn3; 11.  
DR SMART: SM00058; FN1; 3.  
DR SMART: SM00060; FN3; 9.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01253; FIBRONECTIN\_1; 1.  
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;  
KW Repeat. 1 1  
PT NON\_TER

[illegible]

RESULT 7			
FINC_XENLA			
ID	FINC_XENLA	STANDARD:	PRT: 2481 AA.
AC	Q91740;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Fibroectin precursor.		
DE	Fibroectin precursor.		
GN	FN1.		
OS	Xenopus laevis (African clawed frog).		
OS	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
NCBI	_taxid=8355;		



OY 121 IRHHPEFGSPREDRVPHSRNSITLTLNLPGEYVAVSYALNGRESPLLIGQSTVSD 180  
 DB 1481 IRKQESGAGRKEERVPSPRSNITLHLPGSEYLVSTIANGQOESLPLAQOATVSD 1540  
 OY 181 VPRLDEVATPTSLTISMDAPAVTVRYRITYTGETGNSPVOEFTVPGSKSTATISGLK 240  
 DB 1541 VPRLDEVATPTSLTISMDAPAVTVRYRITYTGETGNSPVOEFTVPGSKSTATISGLK 240  
 OY 241 PGVDYITTYAATGRCDSRSPASPKPISINRTETIDKP-SNAGSI 283  
 DB 1601 PGVSYITTYAATGRCDSRSPASPKPILIIHKTDQPIDMAVTDI 1644  
 RESULT 8  
 FGF2\_HUMAN  
 ID FGF2\_HUMAN STANDARD: PRT: 155 AA.  
 AC P09038;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatoplin).  
 GN FGF2 OR FGFb.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Friedman J., Gospodarowicz D., Fiddes J.C.;  
 RT "Human basic fibroblast growth factor: nucleotide sequence and genomic organization.";  
 RL EMBO J. 5:2523-2528(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;  
 RT "Human basic fibroblast growth factor: nucleotide sequence, genomic organization, and expression in mammalian cells.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Sommer A., Brewer M.T., Thompson R.C., Moscatelli D., Presta M., Rifkin D.B.;  
 RT "A form of human basic fibroblast growth factor with an extended amino terminus.";  
 RL Biochem. Biophys. Res. Commun. 144:543-550(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Kurukawa T., Sasada R., Iwane M., Igarashi K.;  
 RT "Cloning and expression of cDNA encoding human basic fibroblast growth factor.";  
 RL FEBS Lett. 213:189-194(1987).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-89184522; PubMed-2538817;  
 RA Prats H., Kaghad M., Prats A.C., Klagsbrun M., Lelias J.M., Lianzun P., Chalon P., Tauber J.P., Amalric F., Smith J.A., Caput D.;  
 RT "High molecular mass forms of basic fibroblast growth factor are initiated by alternative CUG codons.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1836-1840(1989).  
 RN [6]  
 RP SEQUENCE OF 10-35.  
 RA MEDLINE-86275260; PubMed-3732516;  
 RA Gauschl P., Frater-Schroeder M., Boehlen P.;  
 RT "Partial molecular characterization of endothelial cell mitogens from human brain: acidic and basic fibroblast growth factors.";

RL FEBS Lett. 204:203-207(1986).  
 RN [7]  
 RP SEQUENCE OF 10-39.  
 RX MEDLINE-86186784; PubMed-3964259;  
 RA Gimenez-Gallejo G., Conn G., Hatcher V.B., Thomas K.A.;  
 RT "Human brain-derived acidic and basic fibroblast growth factors: amino terminal sequences and specific mitogenic activities.";  
 RL Biochem. Biophys. Res. Commun. 135:541-548(1986).  
 RN [8]  
 RP SEQUENCE OF 2-22.  
 RX MEDLINE-87156686; PubMed-2435284;  
 RA Story M.T., Esch E., Shinasaki S., Sasse J., Jacobs S.C., Lawson R.K.;  
 RT "Amino-terminal sequence of a large form of basic fibroblast growth factor isolated from human benign prostatic hyperplastic tissue.";  
 RL Biochem. Biophys. Res. Commun. 142:702-709(1987).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE-91195367; PubMed-1707542;  
 RA Eriksson A.E., Cousens L.S., Weaver L.H., Matthews B.W.;  
 RT "Three-dimensional structure of human basic fibroblast growth factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3441-3445(1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE-94004464; PubMed-7691311;  
 RA Eriksson A.E., Cousens L.S., Matthews B.W.;  
 RT "Refinement of the structure of human basic fibroblast growth factor at 1.6-A resolution and analysis of presumed heparin binding sites by selenate substitution.";  
 RL Protein Sci. 2:1274-1284(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RX MEDLINE-91195368; PubMed-1849658;  
 RA Zhang J., Cousens L.S., Barr P.J., Sprang S.R.;  
 RT "Three-dimensional structure of human basic fibroblast growth factor, a structural homolog of interleukin 1 beta.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3446-3451(1991).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE-92121151; PubMed-1769963;  
 RA Ago H., Kitegawa Y., Fujishima A., Matsuura Y., Katsube Y.;  
 RT "Crystal structure of basic fibroblast growth factor at 1.6-A resolution.";  
 RL J. Biochem. 110:360-363(1991).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE-91095983; PubMed-1702556;  
 RA Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T., Hsu B.T., Rees D.C.;  
 RT "Three-dimensional structures of acidic and basic fibroblast growth factors.";  
 RL Science 251:90-93(1991).  
 RN [14]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-97040521; PubMed-8885834;  
 RA Moy F.J., Seddon A.P., Boehlen P., Powers R.;  
 RT "High-resolution solution structure of basic fibroblast growth factor determined by multidimensional heteronuclear magnetic resonance spectroscopy.";  
 RL Biochemistry 35:13552-13561(1996).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC -----  
 DR EMBL: M175599: AAA52534.1: ALT\_INIT.  
 DR EMBL: X04431: CAA28027.1: -  
 DR EMBL: X04432: CAA28028.1: -  
 DR EMBL: X04433: CAA28029.1: -  
 DR EMBL: M27658: AAA52448.1: -  
 DR EMBL: J04513: AAA52553.1: ALT\_INIT.  
 DR PIR: A25824: A25824.  
 DR PIR: A26642: A26642.  
 DR PIR: B24243: B24243.  
 DR PIR: B24301: B24301.  
 DR PIR: B32878: B32878.  
 DR PIR: S00297: S00297.  
 DR PDB: 2EGF: 15-APR-92.  
 DR PDB: 4EGF: 15-JUL-93.  
 DR PDB: 1FCG: 15-JUL-93.  
 DR PDB: 1BFC: 03-APR-96.  
 DR PDB: 1BFF: 16-JUN-97.  
 DR PDB: 1BFG: 31-JAN-94.  
 DR PDB: 2BFG: 30-APR-94.  
 DR PDB: 1BLA: 08-NOV-96.  
 DR PDB: 1BLD: 08-NOV-96.  
 DR Gene: HGNC:3676; FGF2.  
 DR MIM: 134920: -  
 DR InterPro: IPRO02209; HB/F\_growthfact.  
 DR InterPro: IPRO02348; IL1\_HBGF.  
 DR Pfam: PF00167; FGF\_1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR PRODOM: PD000831; HB/F\_growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 DR KW: Growth factor; Mitogen; Angiogenesis; Heparin-binding;  
 DR 3d-structure.  
 FT CHAIN 1 9  
 FT SITE 10 155 HEPARIN-BINDING GROWTH FACTOR 2.  
 FT SITE 46 48 CELL ATTACHMENT SITE (POTENTIAL).  
 FT BINDING 88 90 CELL ATTACHMENT SITE (POTENTIAL).  
 FT BINDING 116 119 HEPARIN (POTENTIAL).  
 FT STRAND 30 34 HEPARIN (POTENTIAL).  
 FT STRAND 35 38  
 FT STRAND 39 43  
 FT STRAND 45 46  
 FT STRAND 49 52  
 FT STRAND 55 56  
 FT STRAND 58 60  
 FT HELIX 62 66  
 FT STRAND 69 70  
 FT STRAND 71 76  
 FT STRAND 77 80  
 FT STRAND 81 85  
 FT STRAND 87 88  
 FT STRAND 91 94  
 FT HELIX 99 101  
 FT STRAND 103 107  
 FT STRAND 109 110  
 FT STRAND 113 117  
 FT STRAND 121 122  
 FT STRAND 124 124  
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 FT STRAND 129 130  
 FT STRAND 132 133  
 FT STRAND 136 138  
 FT HELIX 141 142  
 FT STRAND 144 146  
 FT STRAND 148 152  
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 Best Local Similarity 99.48; Pred. No. 1.8e-52;

Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 278 MAAAGSTTTLPALEPDGSGAPPGHFKDPKRLCYCKNGGFELRHPPGRVDGVRKSDPHI 337  
 DB 1 MAAAGSTTTLPALEPDGSGAPPGHFKDPKRLCYCKNGGFELRHPPGRVDGVRKSDPHI 60  
 OY 338 KIQLQAEERGVSVIKVCANRILAMKEDGRLASKVYTBCEFFERLENNNTYRSKY 397  
 DB 61 KIQLQAEERGVSVIKVCANRILAMKEDGRLASKVYTBCEFFERLENNNTYRSKY 120  
 OY 398 TSWYVALKRTGQYKLGSKTGPGOKAILPLPMSAAS 432  
 DB 121 TSWYVALKRTGQYKLGSKTGPGOKAILPLPMSAAS 155  
 RESULT 9  
 FGF2\_BOVIN STANDARD; PRT; 155 AA.  
 ID FGF2\_BOVIN STANDARD; PRT; 155 AA.  
 AC P03969;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast  
 DE growth factor) (BGF) (Prostatropin) [Contains: Kidney-derived growth  
 DE factor].  
 GN FGF2 OR FGF-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN 11  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=86261806; PubMed=2425435;  
 RA Abraham J.A., Mergia A., Tumolo A., Friedland J.,  
 RA Hjertild K.A., Gospodarowicz D., Fiddes J.C.;  
 RT Nucleotide sequence of a bovine clone encoding the angiogenic  
 RT protein, basic fibroblast growth factor.";  
 RL Science 233:545-548(1986).  
 RN 12  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=87217066; PubMed=3472745;  
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;  
 RT Human basic fibroblast growth factor: nucleotide sequence, genomic  
 RT organization, and expression in mammalian cells.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).  
 RN 13  
 RN SEQUENCE OF 10-155.  
 RX MEDLINE=86016731; PubMed=3863109;  
 RA Esch F., Baird A., Boehlen P., Guillemin R.,  
 RA Gospodarowicz D., Guillemin P., Guillemin R.;  
 RT Primary structure of bovine pituitary basic fibroblast growth factor  
 RT (FGF) and comparison with the amino-terminal sequence of bovine brain  
 RT acidic FGF.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6507-6511(1985).  
 RN 14  
 RN SEQUENCE OF 1-9.  
 RX MEDLINE=86295737; PubMed=3741423;  
 RA Ueno N., Baird A., Esch F., Ling N., Guillemin R.;  
 RT "Isolation of an amino terminal extended form of basic fibroblast  
 RT growth factor.";  
 RL Biochem. Biophys. Res. Commun. 138:580-588(1986).  
 RN 15  
 RN SEQUENCE OF 25-41.  
 RX MEDLINE=86095426; PubMed=4081126;  
 RA Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;  
 RT "Isolation and partial characterization of an endothelial cell growth  
 RT factor from the bovine kidney: homology with basic fibroblast growth  
 RT factor.";  
 RL Regul. Pept. 12:201-213(1985).  
 RN 16  
 RN SEQUENCE OF 21-40.

RC TISSUE=Kidney;  
 RA MEDLINE=87119165; PubMed=3809608;  
 RX Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Guillemin R.;  
 RT "Purification and partial characterization of a mitogenic factor from  
 RT bovine liver: structural homology with basic fibroblast growth  
 RT factor.";  
 RL Regul. Pept. 16:135-145(1986).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RA MEDLINE=91095983; PubMed=1702556;  
 RX Zhu X., Komiyama H., Chirino A., Faham S., Fox G.M., Arakawa T.,  
 RA Hsu B.-T., Rees D.C.;  
 RT "Three-dimensional structures of acidic and basic fibroblast growth  
 RT factors.";  
 RL Science 251:90-93(1991).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND  
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
 CC AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC -----  
 DR EMBL: M13440; AAA30518.1; -  
 DR PIR: A24663; GKBOB.  
 DR PIR: A24819; A24819.  
 DR PIR: A32878; A32878.  
 DR PDB: 1BAS; 31-OCT-93.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 DR Pfam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR ProDom: PD000831; HB/F\_growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding;  
 KW 3D-structure.  
 KM  
 FT PROPEP 1 9  
 FT CHAIN 10 155 HEPARIN-BINDING GROWTH FACTOR 2.  
 FT SITE 25 155 KIDNEY-DERIVED GROWTH FACTOR.  
 FT SITE 46 48 CELL ATTACHMENT SITE (POTENTIAL).  
 FT SITE 88 90 CELL ATTACHMENT SITE (POTENTIAL).  
 FT BINDING 27 31 HEPARIN (POTENTIAL).  
 FT BINDING 116 119 HEPARIN (POTENTIAL).  
 FT BINDING 30 34  
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 FT STRAND 91 94  
 FT HELIX 99 101  
 FT STRAND 103 107  
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 FT TURN 121 122  
 FT STRAND 124 124

FT STRAND 127 127  
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 FT STRAND 133 133  
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 FT TURN 141 142  
 FT HELIX 144 146  
 FT STRAND 148 151  
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 QY 278 MAAGSTTLPALPEDGSGAFPFGHFKDPRLCKNGGFEFLRHPDGRVGVREKSDPHI 337  
 DB 1 MAAGSTTLPALPEDGSGAFPFGHFKDPRLCKNGGFEFLRHPDGRVGVREKSDPHI 60  
 QY 338 KLOLQAEERGVSVIKVCANRYLAMKEDGRLASKCTDECFEERLESNNYTSRKY 397  
 DB 61 KLOLQAEERGVSVIKVCANRYLAMKEDGRLASKCTDECFEERLESNNYTSRKY 120  
 QY 398 TSNVVALKRTGYKLGSKTGPQKAILFLPMSAAS 432  
 DB 121 SSVYVALKRTGYKLGKTPGQKAILFLPMSAKS 155  
 RESULT 10  
 FGF2\_SHEEP  
 ID FGF2\_SHEEP STANDARD; PRT; 155 AA.  
 AC P20003;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast  
 DE growth factor) (BFGF) (Prostatropin).  
 GN FGF2 OR FGF-2.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sutton R., Ward W.G., Raphael K.A., Cam G.R.;  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 9-155.  
 RX MEDLINE=88055577; PubMed=3678486;  
 RA Simpson R.J., Moritz R.L., Lloyd C.J., Fabri L.J., Nice E.C.,  
 RA Rubira M.R., Burgess A.W.;  
 RT "Primary structure of ovine pituitary basic fibroblast growth  
 RT factor.";  
 RL FEBS Lett. 224:128-132(1987).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND  
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
 CC AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC -----  
 DR EMBL: L36136; AAA31519.1; -  
 DR PIR: S00185; S00185.  
 DR HSSP: P09038; 1BFF.

DR InterPro: IPR002209; HB/F-growthfact.  
 DR InterPro: IPR002348; ILI\_HBGF.  
 DR Pfam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; ILI\_HBGF.  
 DR ProDom: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 KN PROPEP 1 155  
 FT CHAIN 10 155  
 FT SITE 45 48  
 FT BINDING 87 90  
 FT BINDING 27 31  
 FT BINDING 116 119  
 SQ SEQUENCE 155 AA: 17280 MW: 5572364Ba610606D CRC64;

Query Match 33.6%; Score 805; DB 1; Length 155;  
 Best Local Similarity 97.4%; Pred. No. 2.2e-51;  
 Matches 151; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

278 MAAGSITTLPALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVREKSDPHI 337  
 1 MAAGSITTLPALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVREKSDPHI 60  
 338 KQLQAEERGVSVIKGVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRY 397  
 61 KQLQAEERGVSVIKGVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRY 120  
 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432  
 121 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 155

RESULT 11  
 REF2\_RAT 1  
 ID FGF2\_RAT STANDARD: PRT: 154 AA.

AC P13109;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).  
 GN FGF2 OR FGF-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 RN SEQUENCE FROM N.A.  
 RX STRAIN-Sprague-Dawley; TISSUE-Ovary;  
 RA MEDLINE=89061721; PubMed=3196337;  
 RA Shimazaki S., Emoto N., Koba A., Mercado M., Shibata F.,  
 RA Cooksey K., Baird A., Ling N.,  
 RA "Complementary DNA cloning and sequencing of rat ovarian basic fibroblast growth factor and tissue distribution study of its mRNA.";  
 RL Biochem. Biophys. Res. Commun. 157:256-263(1988).  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RC MEDLINE=88262516; PubMed=3387229;  
 RA Kurokawa T., Seno M., Igarashi K.,  
 RA "Nucleotide sequence of rat basic fibroblast growth factor cDNA.";  
 RL Nucleic Acids Res. 16:5201-5201(1988).  
 RN SEQUENCE OF 1-28 FROM N.A.  
 RP STRAIN-Sprague-Dawley; TISSUE-Testis;  
 RX MEDLINE=97200905; PubMed=9048734;  
 RA Pasumartchi K.B.S., Jin Y., Cattini P.A.,  
 RA "Cloning of the rat fibroblast growth factor-2 promoter region and its response to mitogenic stimuli in glioma C6 cells.";  
 RL J Neurochem. 68:898-908(1997).  
 RN SEQUENCE OF 35-154 FROM N.A.

RC STRAIN-Sprague-Dawley; TISSUE-Brain;  
 RX MEDLINE=92329546; PubMed=1378302;  
 RA El-Husseini A.E.-D., Paterson J.A., Myal Y., Shiu R.P.C.,  
 RT "PCR detection of the rat brain basic fibroblast growth factor (bFGF) mRNA containing a unique 3' untranslated region.";  
 RL Biochem. Biophys. Acta 1131:314-316(1992).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- SUBUNIT MONOMER.  
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES EXAMINED.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC EMBL: M22427; AAA1210.1; -  
 CC EMBL: X07285; CAA30265.1; -  
 CC EMBL: U78079; AAC53225.1; -  
 CC EMBL: X61697; CAA3863.1; -  
 CC PIR: S00876; S00876.  
 CC PIR: A31674; A31674.  
 CC HSSP: P09038; 1BFF.  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DR InterPro: IPR002348; ILI\_HBGF.  
 DR Pfam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; ILI\_HBGF.  
 DR ProDom: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 FT PROPEP 1 9  
 FT CHAIN 10 154  
 FT BINDING 26 30  
 FT BINDING 115 118  
 SQ SEQUENCE 154 AA: 17139 MW: 1A0F14FF423D8403 CRC64;

Query Match 33.0%; Score 792.5; DB 1; Length 154;  
 Best Local Similarity 96.1%; Pred. No. 1.7e-50;  
 Matches 149; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 278 MAAGSITTLPALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVREKSDPHI 337  
 DB 1 MAAGSITTLPALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVREKSDPHI 59  
 QY 338 KQLQAEERGVSVIKGVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRY 397  
 DB 60 KQLQAEERGVSVIKGVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRY 119

QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432  
 DB 120 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 154  
 RESULT 12  
 REF2\_MOUSE 1  
 ID FGF2\_MOUSE STANDARD: PRT: 154 AA.  
 AC P15655;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).  
 GN FGF2 OR FGF-2.  
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=90201563; PubMed=2318343;  
 RT Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;  
 RT "Isolation of cDNAs encoding four mouse EGF family members and  
 RT characterization of their expression patterns during embryogenesis.";  
 RL Dev. Biol. 138:454-463(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57Bl/6J, A/J, and NOD/LtJ; TISSUE=Spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND  
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -I- SUBUNIT: MONOMER.  
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
 CC AFGF.  
 CC -I- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: M30644; AAA37621.1; -  
 DR EMBL: AF065903; AAC17503.1; -  
 DR EMBL: AF065904; AAC17504.1; -  
 DR EMBL: AF065905; AAC17505.1; -  
 DR PIR: C37360; C37360.  
 DR HSSP: P09038; 1BPF.  
 DR MGI: MGI:95516; Fgf2.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 DR Pfam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR ProDom: PD000831; HB/F\_growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 FT PROPEP 1 9  
 FT CHAIN 10 154 HEPARIN-BINDING GROWTH FACTOR 2.  
 FT BINDING 26 30 HEPARIN (POTENTIAL).  
 FT BINDING 115 118 HEPARIN (POTENTIAL).  
 FT BINDING 115 118 HEPARIN (POTENTIAL).  
 FT BINDING 115 118 HEPARIN (POTENTIAL).  
 SQ SEQUENCE 154 AA: 17153 MW: 6895677416274388 CRC64;  
 Query Match 32.4%; Score 777.5; DB 1; Length 154;  
 Best Local Similarity 94.2%; Pred. No. 2e-49; Mismatches 5; Indels 1; Gaps 1;  
 Matches 146; Conservative 5; Mismatches 3; Indels 1; Gaps 1;  
 QY 278 MAAGSTTLPALPEDGSGAFPPGHHKDPKRLCYCKNGGFLLRIHPDGRVDGVRKSDPH 337  
 DB 1 MAAGSTTLPALPEDGSGAFPPGHHKDPKRLCYCKNGGFLLRIHPDGRVDGVRKSDPH 59  
 QY 338 KTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 397  
 DB 60 KTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 119  
 QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432  
 DB 120 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 154  
 RESULT 13  
 ID FGF2\_MONDO STANDARD; PRT; 156 AA.

AC P48798;  
 DT 01-FEB-1996 (rel. 33, Last sequence update)  
 DT 01-FEB-1996 (rel. 33, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast  
 DE growth factor) (BRGF) (Prostatoplin).  
 GN FGF2.  
 OS Monodelphis domestica (Short-tailed grey opossum).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.  
 CC NCBI\_TaxID=13616;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=94296558; PubMed=8024698;  
 RA Kuswilt D.F., Sabourin C.L.K., Sherburn T.E., Ley R.D.;  
 RT "Characterization of cDNA encoding basic fibroblast growth factor of  
 RT the marsupial Monodelphis domestica.";  
 RL DNA Cell Biol. 13:549-554(1994).  
 CC -I- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND  
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -I- SUBUNIT: MONOMER.  
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
 CC AFGF.  
 CC -I- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: Z15154; CA78854.1; ALT\_INIT.  
 DR HSSP: P09038; 1BPF.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 DR Pfam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR ProDom: PD000831; HB/F\_growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 FT PROPEP 1 9  
 FT CHAIN 10 156 HEPARIN-BINDING GROWTH FACTOR 2.  
 FT BINDING 28 32 HEPARIN (POTENTIAL).  
 FT BINDING 117 120 HEPARIN (POTENTIAL).  
 FT BINDING 117 120 HEPARIN (POTENTIAL).  
 SQ SEQUENCE 156 AA: 17303 MW: 7655FCC49BF1209 CRC64;  
 Query Match 31.5%; Score 754.5; DB 1; Length 156;  
 Best Local Similarity 92.3%; Pred. No. 9.4e-48; Mismatches 6; Indels 1; Gaps 1;  
 Matches 144; Conservative 5; Mismatches 6; Indels 1; Gaps 1;  
 QY 278 MAAGSTTLPALPEDGSGAFPPGHHKDPKRLCYCKNGGFLLRIHPDGRVDGVRKSDPH 336  
 DB 1 MAAGSTTLPALPEDGSGAFPPGHHKDPKRLCYCKNGGFLLRIHPDGRVDGVRKSDPH 60  
 QY 337 IKTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 396  
 DB 61 IKTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 120  
 QY 397 YTSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432  
 DB 121 YTSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 156  
 RESULT 14  
 ID FGF2\_CHICK STANDARD; PRT; 158 AA.

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF).  
 GN FGF2 OR FGF-2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 NCBI\_TaxID=9031;  
 RX MEDLINE=93246053; PubMed=7683281;  
 RA Borth A, Zeller R, Meijers C;  
 RT "Expression of alternatively spliced bFGF first coding exons and antisenase mRNAs during chicken embryogenesis.";  
 RL Dev. Biol. 157:110-118(1993).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC  
 CC EMBL: M95707; AAA48617.1; -  
 DR HSSP: P09038; 1BFF.  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DR Pfam: PR00167; FGF\_1  
 DR PRINTS: PR00267; ILIHGF.  
 DR PRODOM: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 KM Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 FT PROPEP 1 12  
 FT CHAIN 13 158  
 FT BINDING 30 34  
 FT BINDING 119 122  
 SEQUENCE 158 AA: 17374 MW: 7869864 C17F1816 CRC64;  
 Query Match 31.4%; Score 753; DB 1; Length 158;  
 Best Local Similarity 91.6%; Pred. No. 1.2e-47;  
 Matches 141; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 279 AASITTLPLPDPGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIK 338  
 DB 5 AASITTLPLPDPGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIK 64  
 QY 339 LQLOAERGVSVIKGVCANRYLAKKEDGRLLASKCVDCEFFERLESNNYTRSKRYT 398  
 DB 65 LQLOAERGVSVIKGVCANRYLAKKEDGRLLASKCVDCEFFERLESNNYTRSKRYT 124  
 QY 399 SWYVALKRTGQYKLGSKTGPQKAILFLPMSAAS 432  
 DB 125 DWYVALKRTGQYKLGSKTGPQKAILFLPMSAAS 158  
 RESULT 15  
 FGF2\_RABBIT STANDARD: PRT: 137 AA.  
 ID FGF2\_RABBIT  
 AC P48799;  
 DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Heparin-binding growth factor 2 (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin) (Fragment).  
 GN FGF2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 RX MEDLINE=93343209; PubMed=8342599;  
 RA Winkles J.A., Priesel R., Alberts G.F., Janat M.F., Liau G.;  
 RT "Elevated expression of basic fibroblast growth factor in an immortalized rabbit smooth muscle cell line.";  
 RL Am. J. Pathol. 143:518-527(1993).  
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
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 CC  
 CC EMBL: I12034; AAA31248.1; -  
 DR HSSP: P09038; 1BFF.  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DR Pfam: PR00167; FGF\_1  
 DR PRODOM: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 KM Growth factor; Mitogen; Angiogenesis; Heparin-binding.  
 FT BINDING 18 22  
 FT BINDING 107 110  
 FT NON\_TER 137 137  
 SEQUENCE 137 AA: 15418 MW: 15418 MW: 0D9DE457B88E8C51 CRC64;  
 Query Match 30.8%; Score 738; DB 1; Length 137;  
 Best Local Similarity 99.3%; Pred. No. 1.2e-46;  
 Matches 136; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 287 PALPEGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIKLOAER 346  
 DB 1 PALPEGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIKLOAER 60  
 QY 347 GYVSTIGVCANRYLAKKEDGRLLASKCVDCEFFERLESNNYTRSKRYTSMYVALKR 406  
 DB 61 GYVSTIGVCANRYLAKKEDGRLLASKCVDCEFFERLESNNYTRSKRYTSMYVALKR 120  
 QY 407 TGOYKLGSKTGPQKAI 423  
 DB 121 TGOYKLGSKTGPQKAI 137  
 Search completed: March 13, 2003, 09:26:25  
 Job time : 37 secs



GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 06:13:37 ; Search time 73 Seconds  
(without alignments)  
1289.911 Million cell updates/sec

Title: US-09-775-964-5

Perfect score: 2398

Sequence: 1 PTDLRFNIGPDMRTVWAP.....LVTLPHNLMHGPETLDVPST 457

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	824.5	34.4	196	4 P78443	P78443 homo sapien
2	762	31.8	153	4 Q925A3	Q925A3 mus musculu
3	760.5	31.7	2478	11 Q93406	Q93406 brachydanio
4	740.5	30.9	170	11 Q60487	Q60487 cavia porce
5	698	29.1	155	13 Q90Y92	Q90Y92 cynops pyrr
6	676	28.2	130	6 Q77767	Q77767 cynops pyrr
7	618	25.8	135	13 Q8QFR9	Q8QFR9 canis famli
8	585	24.4	111	6 Q9BDX1	Q9BDX1 fugu rubrip
9	561	23.4	108	6 Q9N1S7	Q9N1S7 capreolus c
10	561	23.4	125	13 Q98TP8	Q98TP8 cynops pyrr
11	484	20.2	109	11 Q925A1	Q925A1 mus musculu
12	480	20.0	112	11 Q925A2	Q925A2 mus musculu
13	476	19.8	101	13 P79706	P79706 cynops pyrr
14	474.5	19.8	146	13 Q07659	Q07659 gallus gall
15	457	19.1	87	6 Q8WMP4	Q8WMP4 equus cabal
16	428.5	17.9	379	4 Q95617	Q95617 homo sapien

17	417	17.4	293	6 Q9XSG0	Q9XSG0 oryctolagus
18	415.5	17.3	810	11 Q8R3F3	Q8R3F3 mus musculu
19	394	16.4	712	4 Q00531	Q00531 homo sapien
20	394	16.4	4	Q92752	Q92752 homo sapien
21	394	16.4	4	Q15568	Q15568 homo sapien
22	383.5	16.0	354	4 Q9UQ56	Q9UQ56 homo sapien
23	378.5	15.8	1356	11 Q05546	Q05546 rattus norv
24	358	14.9	1353	13 Q00546	Q00546 rattus norv
25	341	14.2	76	6 Q9N0V2	Q9N0V2 ovus aries
26	336	14.0	1532	13 Q90994	Q90994 gallus gall
27	332.5	13.9	114	4 Q16443	Q16443 homo sapien
28	332.5	13.9	114	4 Q00527	Q00527 homo sapien
29	329	13.7	1810	13 Q90824	Q90824 gallus gall
30	327	13.6	2019	11 Q64706	Q64706 mus musculu
31	326.5	13.6	614	13 Q90484	Q90484 brachydanio
32	325	13.6	1294	4 Q9UQP3	Q9UQP3 homo sapien
33	323.5	13.5	592	4 Q95697	Q95697 homo sapien
34	318	13.3	619	11 Q62701	Q62701 rattus norv
35	317	13.2	1714	13 Q90995	Q90995 gallus gall
36	312.5	13.0	922	13 Q93405	Q93405 brachydanio
37	309	12.9	654	4 Q00210	Q00210 homo sapien
38	308.5	12.9	347	4 Q96KP9	Q96KP9 homo sapien
39	306.5	12.8	347	6 Q95KV5	Q95KV5 bos taurus
40	305	12.7	68	6 Q28692	Q28692 oryctolagus
41	302.5	12.6	4135	6 Q18977	Q18977 bos taurus
42	301	12.6	272	4 Q9H1P7	Q9H1P7 homo sapien
43	299	12.5	672	4 Q60782	Q60782 homo sapien
44	297.5	12.4	843	4 Q05707	Q05707 homo sapien
45	292	12.2	106	6 Q9N1S8	Q9N1S8 capreolus c

## ALIGNMENTS

## RESULT 1

ID	P78443	PRELIMINARY:	PRT:	196 AA.
AC	P78443:			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	21 kDa basic fibroblast growth factor (BFGF).			
GN	FGF2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89184522; PubMed=2538817;			
RA	Pirats H., Kagnad M., Pirats A.C., Klagsbrun M., Lelias J.M.,			
RA	Liauzun P., Chalou P., Tauber J.P., Amarlic F., Smith J.A., Caput D.;			
RT	"High molecular mass forms of basic fibroblast growth factor are			
RT	initiated by alternative CUG codons.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1836-1840(1989).			
RN	[2]			
RP	SEQUENCE OF 81-168 FROM N.A.			
RX	MEDLINE=93038590; PubMed=1417798;			
RA	Watson R., Anthony F., Pickett M., Lambden P., Masson G.M.,			
RA	Thomas E.J.;			
RT	"Reverse transcription with nested polymerase chain reaction shows			
RT	expression of basic fibroblast growth factor transcripts in human			
RT	granulosa and cumulus cells from in vitro fertilisation patients.";			
RT	Biochem. Biophys. Res. Commun. 187:1227-1231(1992).			
DR	EMBL; J04513; AAA52532.1; -			
DR	EMBL; S47380; AADI3853.1; -			
DR	HSSP; P09038; 1BPF.			
DR	InterPro; IPR002209; HB/F-growthfact.			
DR	InterPro; IPR002348; IL1_HBGF.			
DR	Pfam; PF00167; FGF; 1.			
DR	PRINTS; PR00262; IL1HBGF.			
DR	ProDom; PD000831; HB/F-growthfact; 1.			
DR	SMART; SM00442; FGF; 1.			

ID	PROSITE: PS00247; HBGF_EGF.1.	DB5447137E60343	CRC64:
DR	SEQUENCE	196 AA; 21203 MW;	
QY	Query Match	34.4%; Score 824.5; DB 4;	Length 196;
DB	Best Local Similarity	88.8%; Pred. No. 4.5e-54;	
DB	Matches 159; Conservative	4; Mismatches 15; Indels	1; Gaps
QY	254 GCGDPSAPSKPTISINRTMRIDKPSMAAGSITLPAIPEDGSGAPPGGFKPKRLCYCN	313	
DB	19 GCGTAPRAAPAPARSGREG-PAGTMAAGSITLPAIPEDGSGAPPGGFKPKRLCYCN	77	
QY	314 GGFELRIHPDGVYDGVREKSDPHIKLOLAEEGVYSISGVCANRYLAKEDGRLLASKC	373	
DB	78 GGFELRIHPDGVYDGVREKSDPHIKLOLAEEGVYSISGVCANRYLAKEDGRLLASKC	137	
QY	374 VTDECFEERLESNNNTYRSRRKYTSWYVALKRTGOYKLGSKTGPQAKILFLPMSAKS	432	
DB	138 VTDECFEERLESNNNTYRSRRKYTSWYVALKRTGOYKLGSKTGPQAKILFLPMSAKS	196	
QY	2543		
ID	Q925A3	PRELIMINARY;	PRT; 153 AA.
AC	Q925A3:		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Fibroblast growth factor 2.		
GN	FGF2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10090;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N;		
RA	Dirks R.P., Griep A.E.		
RT	"Multiple novel variants of fibroblast growth factor 2 transcripts are		
RL	submitted in mouse embryos."		
EMBL	Submitted FEB-2001 to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF027551; AAK52308.1.-.		
DR	InterPro; IPR002209; HB/F-1 growthfact.		
DR	Pfam; PF00167; FGF, 1.		
DR	Pficond; P0000831; HB/F-1 growthfact; 1.		
DR	SEQUENCE 153 AA; 17024 MW; A08163CDBFA2PAAB		
DR	CRC64;		
QY	Query Match	31.8%; Score 762; DB 11;	Length 153;
DB	Best Local Similarity	93.5%; Pred. No. 1.5e-49;	
DB	Matches 145; Conservative	5; Mismatches 3; Indels	2; Gaps
QY	278 MAAGSITLPAIPEDGSGAPPGGFKPKRLCYCNKGFFELRIHPDGVYREKSDPHI	337	
DB	1 MAAGSITLPAIPEDGSGA-APPGGFKPKRLCYCNKGFFELRIHPDGVYREKSDPHI	59	
QY	338 KLOLAEEGVYSISGVCANRYLAKEDGRLLASCVTECEFFELLESNNNTYRSRY	397	
DB	60 KLOLAEEGVYSISGVCANRYLAKEDGRLLAS-CVTECEFFELLESNNNTYRSRY	118	
QY	398 TSMYVALKRTGOYKLGSKTGPQAKILFLPMSAKS	432	
DB	119 TSMYVALKRTGOYKLGSKTGPQAKILFLPMSAKS	153	
QY	2543		
ID	Q93406	PRELIMINARY;	PRT; 2478 AA.
AC	Q93406:		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Fibronectin.		
GN	FN1.		
OS	Brachydanio rerio (zebrafish) (zebra danio).		

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP  
RA Zebrafish, *Danio rerio* (Gaster, 1858) (Zebrafish, *Danio rerio* (Gaster, 1858))  
RT Characterization and expression of zebrafish fibronectin.  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBS databases.  
DR EMBL: AF081128; AAC31947.1; ..  
DR HSSP: P02751; IEBR.  
DR ZFIN: ZDB-GENE-000426-1; fn1.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000083; Fibnrcn1.  
DR InterPro: IPR003962; fn1n1\_repeat.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR000562; FN\_Type\_II.  
DR Pfam: PF000039; fn1; 12.  
DR Pfam: PF000040; fn2; 2.  
DR Pfam: PF00041; fn3; 17.  
DR Pfam: PF00012; FNYPEI.  
DR PRINTS: PR00013; FNYPEII.  
DR PRINTS: PR00014; FNYPEIII.  
DR ProDom: PD000995; FN\_Type\_II; 2.  
DR SMART: SM00058; FN1; 12.  
DR SMART: SM00059; FN2; 2.  
DR SMART: SM00060; FN3; 14.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01253; FIBRONECTIN\_1; UNKNOWN\_11.  
DR PROSITE: PS00023; FIBRONECTIN\_2; 2.  
KW Repeat.  
SQ  
SEQUENCE 2478 AA: 271652 MW: A03475C55A385750 CAC64:  
  
Query Match 31.7%; Score 760.5; DB: 13; Length 2478;  
Best Local Similarity 54.3%; Pred. NO. 9.8e-48;  
Matches 152; Conservative 45; Mismatches 78; Indels 5; Gaps 4.  
  
OY 1 PTDLPFNIGPDTMRVW-AP--PSSIDLINLVARYSVKNEEDVAVELISPSDNAYVL 57  
Db 1359 PYGSEFEVAVDMLVWAKAPQPKSSDINOIIRHHVDDDDDETEKTVGSENFVLR 1418  
OY 58 NLPFGTEVYVSSVYEQHESTPLRLGROROKTGIDSPETGIDFSDITANSFTYHMIAPRAT 117  
Db 1419 HLVENTLEYLVSVYEGRGSPALIDRELFL-MPCQLQFSFDVGTSTYRWMAAPRAIIS 1477  
OY 118 GYRIHMRPHFSGRPREDRVPHRSNITLTNLTPTETVSVIALNGREESPLIGQOST 177  
Db 1478 GYRIIRYOMTS-GRRAKEERLPBSRHFLLTGLTPTETVSVIYAVSGSRDPLPTGTOST 1536  
OY 178 VSDPRLPEVVAATPNSLISMDAPAVTVRYRYRTYGETGSGNSPVQGFETVPGSKSTATIS 237  
Db 1537 ISDAPDLTEISSSTPSITVRMAPSVTVRYRYRTYHGGSGSDAPLEPWPQGSSTATIE 1596  
OY 238 GLKPGVDYTTVAVATGRGSPASSPSPIINRYETIDPS 277  
Db 1597 DLRGTDYITLVAVATGRGSPASSPSPIINRYETIDPS 1636  
  
RESULT 4  
060487  
ID 060487; PRELIMINARY; PRT: 170 AA.  
AC 060487;  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
DE Fibroblast growth factor 2 (FGF-2) (Fibroblast growth factor, basic)  
DE (bBGF) (Heparin-binding growth factor 2) (bBGF-2) (Prostatotropin)  
DE (Prostatic growth factor) (Fragments).  
DE FGF2.  
SN Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriooanathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;

RN [1] SEQUENCE OF 53-170 FROM N.A.  
 RP TISSUE-PROSTATE;  
 RA Ricciardelli C.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF N-TERMINUS, PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING.  
 RX MEDLINE=8927358; PubMed=2730645;  
 RA Sommer A., Moscattelli D., Rifkin D.B.;  
 RT "An amino-terminally extended and post-translationally modified form  
 of a 25KD basic fibroblast growth factor.";  
 RL Biochem. Biophys. Res. Commun. 160:1267-1274(1989).  
 RN [3]  
 RP PARTIAL SEQUENCE, AND METHYLATION.  
 RX MEDLINE=91322114; PubMed=1713785;  
 RA Burgess W.H., Bizik J., Mehlman J., Quarto N., Rifkin D.B.;  
 RT "Direct evidence for methylation of arginine residues in high  
 molecular weight forms of basic fibroblast growth factor.";  
 RL Cell Regul. 2:87-93(1991).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX TISSUE-BRAIN;  
 RX MEDLINE=87289686; PubMed=3475702;  
 RA Moscattelli D., Joseph-Silverstein J., Manojas R., Rifkin D.B.;  
 RT "Mr 25,000 heparin-binding protein from guinea pig brain is a high  
 molecular weight form of basic fibroblast growth factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5778-5782(1987).  
 CC -1- FUNCTION: WIDE-SPECTRUM MITOGENIC, ANGIOGENIC, AND NEUROTROPHIC  
 FACTOR. IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC  
 PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND  
 HEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR  
 MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION,  
 PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS  
 SYSTEM AND IN BONE FORMATION. MAJOR ANGIOGENIC FACTOR THAT ALSO  
 ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).  
 CC -1- SUBUNIT: FORMS A QUATERNARY COMPLEX WITH TWO FGFR1 AND AT LEAST  
 ONE HEPARAN SULFATE (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST TWO ISOFORMS: 18 KDA AND 25 KDA  
 (SHOWN HERE); MAY BE PRODUCED BY USE OF ALTERNATIVE TRANSLATION  
 INITIATION SITES. BOTH FORMS ARE ACTIVE.  
 CC -1- PTM: THE N-TERMINAL OF ISOFORM 18 KDA IS BLOCKED (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; MANY FRAMESHIFTS WERE  
 INTRODUCED FROM RESIDUES 77, 88, 93 AND 149 DOWNWARD TO EXTEND THE  
 SIMILARITY TO THE HUMAN SEQUENCE AS WELL AS ON THE BASIS OF  
 PARTIAL AMINO-ACID SEQUENCING.  
 CC EMBL: L75974; AAA85394.1; ALT\_FRAME.  
 DR HSSP; P09038; 1BLA.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR ProDom: PD000831; HB/F\_growthfact; 1.  
 DR SMART; SM00442; FGF; 1.  
 DR PROSITE; PS00247; HBGF\_FGF; 1.  
 KW Growth factor; Mitogen; Vascularization; Heparin-binding;  
 KW Alternative initiation; Methylation; Phosphorylation;  
 KW Non-terminal protein.  
 FT NON\_TER 1  
 FT NON\_CONS 15  
 FT CHAIN 16  
 FT CHAIN <1 170  
 FT INTL\_MOT 22 170  
 FT DOMAIN 11 14  
 FT NON\_CONS 50 51  
 FT SITE 61 63  
 FT SITE 103 105  
 FT BINDING 50 51  
 FT BINDING 105 105  
 FT BINDING 143 159  
 FT MOD\_RES 4 4  
 FT MOD\_RES 6 6  
 FT MOD\_RES 8 8  
 FT MOD\_RES 88 88  
 FT MOD\_RES 88 88  
 25 KDA BASIC FIBROBLAST GROWTH FACTOR.  
 18 KDA BASIC FIBROBLAST GROWTH FACTOR.  
 FOR 18 KDA FORM.  
 POLY-ALA.  
 CELL ATTACHMENT SITE (POTENTIAL).  
 CELL ATTACHMENT SITE (POTENTIAL).  
 HEPARIN (BY SIMILARITY).  
 HEPARIN (BY SIMILARITY).  
 HEPARIN (BY SIMILARITY).  
 METHYLATION (MONO- OR DI-).  
 METHYLATION (MONO- OR DI-).  
 METHYLATION (MONO- OR DI-).  
 PHOSPHORYLATION (BY SIMILARITY).

FT MOD\_RES 136 136 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 170 AA; 18354 MW; F36BDBDC736E5FEBE CRC64;  
 Query Match 30.9%; Score 740.5; DB 11; Length 170;  
 Best Local Similarity 80.7%; Pred. No. 7.2e-48;  
 Matches 146; Conservative 8; Mismatches 8; Indels 19; Gaps 3;  
 QY 254 GGGDSVASSKPSINRTFLDKP--SMAGSTITTPALPEGGSSGAFPPGCHKDRRLK 311  
 DB 7 GRTAAARR-----EPGMAAGSTITTPALPEGGGGAFAFGHRRDP----- 50  
 QY 312 KNGGFLRLHPDGRVDGVRKSDPHIKLOLAEEGVSIKGCARRYLAMKEDGRLLAS 371  
 DB 51 -NGGFLRLHPDGRVDGVRKSDPHIKLOLAEEGVSIKGCARRYLAMKEDGRLLAS 109  
 QY 372 KCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGYKLGSKTGPGGKAILFLPMSAA 431  
 DB 110 KCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGYKLGSKTGPGGKAILFLPMSAK 169  
 QY 432 S 432  
 DB 170 S 170  
 RESULT 5  
 ID Q90Y92 PRELIMINARY; PRT; 155 AA.  
 AC Q90Y92;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Fibroblast growth factor-2.  
 GN FGF-2.  
 OS Cynops pyrrhogaster (Japanese common newt).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.  
 OX NCBI\_TaxID=8330;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susaki K., Nakamura K., Chiba C., Saito T.;  
 RT "Expression of FGF2 during newt retinal development and  
 regeneration.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB064664; BAB63249.1; -  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR Pfam; PF00167; FGF; 1.  
 DR ProDom: PD000831; HB/F\_growthfact; 1.  
 DR PROSITE; PS00247; HBGF\_FGF; UNKNOWN.1.  
 DR SEQUENCE 155 AA; 17278 MW; 2B583058538AB8D9 CRC64;  
 Query Match 29.1%; Score 698; DB 13; Length 155;  
 Best Local Similarity 85.2%; Pred. No. 9.5e-45;  
 Matches 132; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
 QY 278 MAGSTITTPALPEGGSSGAFPPGCHKDRRLKRYCKNGSGFLRLHPRGVDGVRKSDPHI 337  
 DB 1 MAGSTITTPALPEGGSSGAFPPGCHKDRRLKRYCKNGSGFLRLHPRGVDGVRKSDPHI 60  
 QY 338 KIOLAEEGVSIKGCARRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 397  
 DB 61 KIOLAEEGVSIKGCARRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 120  
 QY 398 TSNYYALKRTGYKLGSKTGPGGKAILFLPMSAAS 432  
 DB 121 SDWYVALKRTGYKLGSKTGPGGKAILFLPMSAKS 155  
 RESULT 6  
 ID Q77767 PRELIMINARY; PRT; 130 AA.  
 AC Q77767;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)

01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Basic fibroblast growth factor (bFGF) (FGF-2) (Heparin-binding growth factor 2) (HMGF-2) (Prostatoplin) (Prostatic growth factor) (Fragment).  
 DE bFGF.  
 GN bFGF.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TROCHTA O.A., JACOBS R.M., LAMARRE J.;  
 RT "The role of bFGF in canine Hemangiosarcoma";  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: WIDE-SPECTRUM MITOGENIC, ANGIOGENIC, AND NEUROPROTECTOR. IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND HEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION, PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS SYSTEM AND IN BONE FORMATION. MAJOR ANGIOGENIC FACTOR THAT ALSO ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).  
 CC -1- SUBUNIT: FORMS A QUATERNARY COMPLEX WITH TWO FGFR1 AND AT LEAST ONE HEPARAN SULFATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
 DR EMBL; AF060562; AAC35912.1; -.  
 DR HSSP; P09038; 1BFF.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; ILL\_HBGF.  
 DR Pfam: PF00167; FGF\_1.  
 DR PRINTS; PR00262; ILLHBGF.  
 DR PRODOM; PD000831; HB/F\_growthfact; 1.  
 DR SMART; SM00442; FGF\_1.  
 DR PROSITE; PS00247; HBGF\_FGF; 1.  
 KW Growth factor; Mitogen; Vascularization; Heparin-binding; Phosphorylation; Developmental protein.  
 FT NON\_TER 1  
 FT SITE 21  
 FT BINDING 63  
 FT BINDING 10  
 FT BINDING 11  
 FT BINDING 65  
 FT BINDING 103  
 FT MOD\_RES 48  
 FT MOD\_RES 96  
 FT NON\_TER 130  
 SQ SEQUENCE 130 AA; 14902 MW; 21900876E878FEAE CRC64;  
 Query Match 28.2%; Score 676; DB 6; Length 130;  
 Best Local Similarity 96.9%; Pred. No. 3,3e-43;  
 Matches 126; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Basic fibroblast growth factor (bFGF) (FGF-2) (Heparin-binding growth factor 2) (HMGF-2) (Prostatoplin) (Prostatic growth factor) (Fragment).  
 DE bFGF.  
 GN bFGF.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TROCHTA O.A., JACOBS R.M., LAMARRE J.;  
 RT "The role of bFGF in canine Hemangiosarcoma";  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: WIDE-SPECTRUM MITOGENIC, ANGIOGENIC, AND NEUROPROTECTOR. IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND HEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION, PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS SYSTEM AND IN BONE FORMATION. MAJOR ANGIOGENIC FACTOR THAT ALSO ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).  
 CC -1- SUBUNIT: FORMS A QUATERNARY COMPLEX WITH TWO FGFR1 AND AT LEAST ONE HEPARAN SULFATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
 DR EMBL; AF060562; AAC35912.1; -.  
 DR HSSP; P09038; 1BFF.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; ILL\_HBGF.  
 DR Pfam; PF00167; FGF\_1.  
 DR PRINTS; PR00262; ILLHBGF.  
 DR PRODOM; PD000831; HB/F\_growthfact; 1.  
 DR SMART; SM00442; FGF\_1.  
 DR PROSITE; PS00247; HBGF\_FGF; 1.  
 FT NON\_TER 1  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA; 12633 MW; EC0967A5261F5487 CRC64;  
 Query Match 24.4%; Score 585; DB 6; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-36;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

01-JUN-2002 (TREMblrel. 17, Last annotation update)  
 DE Basic fibroblast growth factor (bFGF) (FGF-2) (Heparin-binding growth factor 2) (HMGF-2) (Prostatoplin) (Prostatic growth factor) (Fragment).  
 DE bFGF.  
 GN bFGF.  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.  
 NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Botchenby M.R.;  
 RT "Comparative vertebrate genomic sequence analysis studies based on Fugu rubripes";  
 RL Thesis (2001), University College London, London, United Kingdom.  
 DR EMBL; AJ426040; CAD19830.1; -.  
 SQ SEQUENCE 155 AA; 17113 MW; AEFEL2DBDC78FB8E CRC64;  
 Query Match 25.8%; Score 618; DB 13; Length 155;  
 Best Local Similarity 77.1%; Pred. No. 9,2e-39;  
 Matches 118; Conservative 5; Mismatches 30; Indels 0; Gaps 0;

01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Basic fibroblast growth factor (bFGF) (FGF-2) (Heparin-binding growth factor 2) (HMGF-2) (Prostatoplin) (Prostatic growth factor) (Fragment).  
 DE bFGF.  
 GN bFGF.  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Canidae; Canis.  
 NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sekhon H.S., Keller J.R., Spindel E.R.;  
 RT "Alterations in Collagen and Elastin Gene Expression in Fetal Pulmonary Vessels in Monkeys Following Prenatal Nicotine Exposure: A Possible Role of alpha7 Nicotinic Acetylcholine Receptor in Persistent Pulmonary Hypertension";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF251270; MAK37962.1; -.  
 DR HSSP; P09038; 2EFG.  
 DR InterPro: IPR002209; HB/F\_growthfact.  
 DR InterPro: IPR002348; ILL\_HBGF.  
 DR Pfam; PF00167; FGF\_1.  
 DR PRINTS; PR00262; ILLHBGF.  
 DR PRODOM; PD000831; HB/F\_growthfact; 1.  
 DR SMART; SM00442; FGF\_1.  
 DR PROSITE; PS00247; HBGF\_FGF; 1.  
 FT NON\_TER 1  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA; 12633 MW; EC0967A5261F5487 CRC64;  
 Query Match 24.4%; Score 585; DB 6; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-36;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 IHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLASKCVTDEC 60
OY 380 FFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFLPMSA 430
    |||||||
Db 61 FFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFLPMSA 111

RESULT 9
O9N1S7 PRELIMINARY: PRT: 108 AA.
AC O9N1S7:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Basic fibroblast growth factor (Fragment).
CN BGF.
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Capreolus.
NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=20532861; PubMed=11078967;
RA Wagener A., Biotner S., Goritz F., Fickel J.;
RT "Detection of growth factors in the testis of roe deer (Capreolus
RT capreolus).";
RL Annu. Reprod. Sci. 64:65-75(2000).
DR EMBL: AF152587; AAF3226.1; -.
DR HSSP: P09038; 4FGF.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12399 MW; 68C7B7244214567E CRC64;

Query Match
Best Local Similarity 23.4%; Score 561; DB 6; Length 108;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 319 RIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLASKCVTDEC 378
    |||||||
    b 1 RIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLASKCVTDEC 60
OY 379 FFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFL 426
    |||||||
    Db 61 FFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFL 108

RESULT 10
O98TD8 PRELIMINARY: PRT: 125 AA.
AC O98TD8:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Fibroblast growth factor-2 (Fragment).
CN FGF-2.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno N., Hayashi T., Kondo H., Okamoto M.;
RT "Cynops fibroblast growth factor-2.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AB049625; BAB40835.1; -.
DR HSSP: P09038; 1BFP.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 125 AA; 14244 MW; 5C27F41DC6E60C13 CRC64;

Query Match
Best Local Similarity 23.4%; Score 561; DB 13; Length 125;
Matches 107; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 309 LYCKNGGFRLRIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRL 368
    |||||||
    Db 2 LYCKNGGFRLRIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRL 61
OY 369 LASKCVTDECFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFLPM 428
    |||||||
    Db 62 MALKWITDECFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGKAILFLPM 121
OY 429 SAAS 432
    || |
    Db 122 SAKS 125

RESULT 11
O925A1 PRELIMINARY: PRT: 109 AA.
AC O925A1:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Fibroblast growth factor 2.
CN FGF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Dirks R.P., Griep A.E.;
RT "Multiple novel variants of fibroblast growth factor 2 transcripts are
RT expressed in mouse embryos.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY027558; AAK52310.1; -.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOW1.
SQ SEQUENCE 109 AA; 12388 MW; 61074ADE3303C860 CRC64;

Query Match
Best Local Similarity 20.2%; Score 484; DB 11; Length 109;
Matches 93; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 337 IKLQQAEEGVVSIGVCANRYLAMKEDGRLASKCVTDECFFERLESNNYNTYRSRK 396
    |||||||
    Db 14 IKLQQAEEGVVSIGVCANRYLAMKEDGRLASKCVTDECFFERLESNNYNTYRSRK 73
OY 397 YTSWYVALKRTGQYKLGSTGPGKAILFLPMSAAS 432
    |||||||
    Db 74 YTSWYVALKRTGQYKLGSTGPGKAILFLPMSAKS 109

RESULT 12
O925A2

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ID Q925A2 PRELIMINARY; PRT; 112 AA.  
 AC Q925A2:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Fibroblast growth factor 2.  
 GN FGF2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N;  
 RA Dicks R.P., Griep A.E.;  
 RT "Multiple novel variants of fibroblast growth factor 2 transcripts are  
 expressed in mouse embryos."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A1021537; AAK52309.1;  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DE InterPro: IPR002348; IL1\_HBGF.  
 PFam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR PRODOM: PD000831; HB/F-growthfact; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; UNKNOWN; 1.  
 SQ SEQUENCE 112 AA; 12725 MW; B00557ABE0257CCB CRC64;

Query Match 20.0%; Score 480; DB 11; Length 112;  
 Best Local Similarity 96.8%; Pred. No. 1.2e-28;  
 Matches 92; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 338 KIQLQAEERGVVSIKVCANRYIAMKEDGRLLASKCVTDECFEELSENNTYRSRY 397  
 DB 18 KIQLQAEERGVVSIKVCANRYIAMKEDGRLLASKCVTDECFEELSENNTYRSRY 77  
 QY 398 TSMYVALKRTGQYKLGSKTGPQKALFLPMSAAS 432  
 DB 78 TSMYVALKRTGQYKLGSKTGPQKALFLPMSAAS 112

RESULT 13  
 ID P79706 PRELIMINARY; PRT; 101 AA.  
 AC P79706:  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Basic FGF (Fragment).  
 OS Cynops pyrrhogaster (Japanese common newt).  
 OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TaxID=8330;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EMBRYO;  
 RA Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takashima K.,  
 Kaneda T.;  
 RT "Serial expression of the genes in a mesodermalizing ectoderms of  
 early Cynops gastrula."  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D89443; BAA13958.1;  
 DR HSSP: P09038; 4RFG.  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 PFam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR PRODOM: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 101 AA; 11907 MW; 74A16C866C1F457A CRC64;

Query Match 19.8%; Score 476; DB 13; Length 101;  
 Best Local Similarity 87.1%; Pred. No. 2.1e-28;  
 Matches 88; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 306 PKRLXKNGCFELRIHPDGVREKSPDHKIKLQAEERGVVSIKVCANRYIAMKED 365  
 DB 1 PKRLXKNGCFELRIHPDGVREKSPDHKIKLQAEERGVVSIKVCANRYIAMKED 60  
 QY 366 GRLLASKCVTDECFEELSENNTYRSRYTSWYVALKR 406  
 DB 61 GRLLASKCVTDECFEELSENNTYRSRYTSWYVALKR 101

RESULT 14  
 ID Q07659 PRELIMINARY; PRT; 146 AA.  
 AC Q07659:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Fibroblast growth factor.  
 GN BFGF.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=93246053; PubMed=7683281;  
 RA Boria A.Z., Zeller R., Weijers G.;  
 RT "Expression of alternatively spliced bfgf first coding exons and  
 antisense mRNAs during chicken embryogenesis."  
 RL Dev. Biol. 157:110-118(1993).  
 RN [2]  
 RP SEQUENCE OF 52-85 FROM N.A.  
 RX MEDLINE=90382254; PubMed=2401202;  
 RA Mitran E., Gruenbaum Y., Shohat H., Ziv T.;  
 RT "Fibroblast growth factor during mesoderm induction in the early chick  
 embryo."  
 RL Development 109:387-393(1990).  
 DR EMBL: M95706; AAA48616.1;  
 DR EMBL: X56804; CAA40139.1;  
 DR HSSP: P09038; 2BFG.  
 DR InterPro: IPR002209; HB/F-growthfact.  
 DR InterPro: IPR002348; IL1\_HBGF.  
 PFam: PF00167; FGF; 1.  
 DR PRINTS: PR00262; IL1HBGF.  
 DR PRODOM: PD000831; HB/F-growthfact; 1.  
 DR SMART: SM00442; FGF; 1.  
 DR PROSITE: PS00247; HBGF\_FGF; 1.  
 SQ SEQUENCE 146 AA; 16182 MW; A7CB97BCB456E247 CRC64;

Query Match 19.8%; Score 474.5; DB 13; Length 146;  
 Best Local Similarity 58.4%; Pred. No. 4.6e-28;  
 Matches 101; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

QY 260 ASSKPSINIKREIDPKSMAAGSTITLPALEDGSGAEPFGHFKDPKRLYKNGGFELR 319  
 DB 5 ASSQPRG---TAVGAPRVMSPPADVPSPSLPDGV-----LWER 40  
 QY 320 IHDPGRVDGVRKESDPHNIKLOAEERGVVSIKVCANRYIAMKEDGRLLASKCVTDECF 379  
 DB 41 VPPDERVSAM-----VKLOAEERGVVSIKVCANRYIAMKEDGRLLASKCVTDECF 93  
 QY 380 FFERLESNNYNTYRSRYTSWYVALKRTGQYKLGSKTGPQKALFLPMSAAS 432  
 DB 94 FFERLESNNYNTYRSRYTSWYVALKRTGQYKLGSKTGPQKALFLPMSAAS 146

RESULT 15  
 ID Q8WMP4 PRELIMINARY; PRT; 87 AA.  
 Q8WMP4

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AC Q8MMP4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Fibroblast growth factor 2 (Fragment).
GN FGF2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RA Einspanier R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RA Welter H.;
RL Thesis (2002), Department of Physiology, University of Munich,
  Freising, Germany.
DR EMBL: AJ319906; CAC86028.1;
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF_1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 87 AA; 10128 MW; 52382DDF0245739E CRC64;

Query Match          19.18; Score 457; DB 6; Length 87;
Best Local Similarity 98.9%; Pred. No. 4.6e-27;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 318 LRIHPGVRVGVREKSDPHIKLOLAERGVSTIKGVCANRYLAMKEDGRLLASKCVTDE 377
DB 1 LRIHPGVRVGVREKSDPHIKLOLAERGVSTIKGVCANRYLAMKEDGRLLASKCVTDE 60

QY 378 CFFEEERLESNNYNTYRSRKYSWYVAL 404
DB 61 CFFEEERLESNNYNTYRSRKYSWYVAL 87

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 Job time : 81 secs

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